

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 12:51:03 ; Search time 189 Seconds

(without alignment)

683.478 Million cell updates/sec

Title: US-10-686-490D-2

Perfect score: 1509

Sequence: 1 MAQVKANGITLLEYEQEGHHRH.....ERHIFRLIELIAGHAAAAAA 294

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 433378781 residues

Total number of hits satisfying chosen parameters:

2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_GenSeq_21:*

1: GenSeqP19808;*

2: GenSeqP19908;*

3: GenSeqP20008;*

4: GenSeqP20018;*

5: GenSeqP20028;*

6: GenSeqP20038;*

7: GenSeqP20038B;*

8: GenSeqP20048;*

9: GenSeqP20058;*

RESULT 1

ADO26338

ID ADO26338 standard; protein; 294 AA.

XX ADO26338;

AC XX

DT 29-JUL-2004 (first entry)

XX DE Anti-Kaslauskas lipase protein.

XX KW ds; gene; enzyme; anti-Kaslauskas lipase; esterification; hydrolysis; pharmaceutical; agricultural chemical; liquid crystal compound.

XX OS Synthet.

XX PN EP1418237-A2.

XX PD 12-MAY-2004.

XX PF 06-OCT-2003; 2003EP-00022590.

XX PR 16-OCT-2002; 2002DE-01048166.

XX (PARB) BAYER CHEM AG.

XX PA Bosch B, Meissner R, Barendes F, Koch R;

XX PI WPI; 2004-378759/36.

XX DR N-PSDB; ADO26337.

XX DR

PT New nucleic acid encoding anti-Kazlauskas lipase and derived enzymes,

PT useful for stereospecific hydrolysis and synthesis of aralkyl esters,

PT intermediates for pharmaceuticals and plant protection agents.

XX

KW carboxylic ester racemate; hypertension; analapril; captopril.
 XX Acinetobacter calcoaceticus.
 XX WO200133847-A1.
 XX PD 10-MAY-2001.
 XX 01-NOV-2000; 2000WO-KR001243.
 XX PR 01-NOV-1999; 99KR-00047927.
 XX PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
 (BIOH-) BIOHOLDINGS INC.
 XX P1 Kim C., Rhee S., Song K., Lee J., Boyapaty G.;
 XX DR; 2001-316432/33.
 XX Novel esterase derived from *Pseudomonas aeruginosa* useful for producing
 PT optical active carboxylic acids and pharmaceuticals, preferably
 PT hypertension treatments drugs like analapril or captopril.
 XX PS Example 6: Fig 3; 40pp; English.
 XX The present invention describes an esterase (I) derived from *Pseudomonas aeruginosa* which has a sequence comprising 315 amino acids, and produces optical active carboxylic acids and enantiomeric isomers by the asymmetric hydrolysis activity. (I) is useful for producing optical active carboxylic acids, preferably optical active (R)-carboxylic acids from carboxylic acid ester racemates. (I) is useful for the production of various kinds of physiologically active pharmaceuticals, especially hypertension treatments drugs like analapril or captopril. (I) has excellent ability for producing optically active carboxylic acids from carboxylic acid esters. Production of optically active carboxylic acids by (I) is highly more selective, simple and environmentally favourable when compared to conventional techniques. (I) is thermally stable at high temperatures above 70 degrees Celsius. The present sequence represents a carboxyl esterase amino acid sequence given in comparison with the esterase of the present invention.

Sequence 312 AA;
 SQ Query Match 38.9%; Score 586.5; DB 4; Length 312;
 Best Local Similarity 45.1%; Pred. No. 2.3e-53;
 Matches 129; Conservative 54; Mismatches 100; Indels 3; Gaps 3;

Db 24 6 ANGITLEYEQGRHRPHPSMILINGGGQOLIDWPEEFIRGLABERGFRRVICEDNRDAGLS 65

Qy 24 SNGELHVYEGVGNPDPHTILLINGGLAQALFWDFPFCSSLIDGFFYTRFDRDGSK 83

Db 66 66 LEGY-IKKPNTARYLLASNLG-KPRVPYTLDDMDALDTVGMLDALGEESTHVVGVSMGMI 123

Db 84 84 IRHKGKRNLNTKLMSRTFTLGLNGQAGAPYLDMADYDVSILLEAMRKVNIVGASNGMI 143

Qy 124 124 AOTLGAKRIGERVTSLLMTSSENPRMPAPRPOVQLKMRPKSMDEKEWIKYNLELT 183

Db 144 144 AQIAAKTPEKVEKLAMFTSANQPLLPPFPKQPSLIGKPKSSDEDGIIHSLKFEI 203

Db 184 184 IGSPLGLDRKLALD-VRKSISIERCUCPECTOROLAAITLOSSRSYKLLRIAVPTLVISGAE 242

Qy 204 204 IGSSEGYNNYEAATOTARRYQYORSYHAGVQQLQFQIAITCGSLIQLDKQISQPTLVHGSR 263

Db 243 243 DPLLPYQQCQDIAHDHIPGARFELLEGMDHIDPERHIFPLIELIAGH 288

Db 264 264 DRJLJPPSHKAKVAKAIKGAKFELIJQGMGHDIPSHFIPQSYLPAHH 309

Qy 304 304 LGSPGL--DREKLALDVRSKTECLCPEGTORQLAIIOSGRVRLKLRRIAVPTLVISGA 241

Db 304 304 LGSPGL--DREKLALDVRSKTECLCPEGTORQLAIIOSGRVRLKLRRIAVPTLVISGA 241

Qy 242 242 EDPLLPYQQCQDIAHDHIPGARFELLEGMDHIDPERHIFPLIELIAGHAAA 291

AC AC073253;
 XX DT 29-JUL-2004 (first entry)
 XX DE Pseudomonas aeruginosa polypeptide #5428.
 XX KW Bacterial infection; *Pseudomonas aeruginosa* infection; antibacterial.
 XX OS *Pseudomonas aeruginosa*.
 XX PN US6551795-B1.
 XX PD 22-APR-2003.
 XX PP 18-FEB-1999; 99US-00252991.
 XX PR 18-FEB-1998; 98US-0074788P.
 XX PR 27-JUL-1998; 98US-0094190P.
 XX PA (GENO-) GENOME THERAPEUTICS CORP.
 XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX DR; 2003-615309/58.
 XX DR N-PSDB; ABD06824.
 XX PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
 XX PT Disclosure; SEQ ID NO 21999; 455pp; English.
 XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused CC infection, and in detection of *P. aeruginosa* sequences or other sequences CC of *Pseudomonas* species using biochip technology. Sequences ABO67326-CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The CC sequence data for this patent did not form part of the printed CC specification but was obtained in electronic format from USPTO at CC seqdata.uspto.gov/sequence.html
 XX Sequence 422 AA;

Query Match 37.3%; Score 562.5; DB 7; Length 422;
 Best Local Similarity 43.1%; Pred. No. 1.3e-50;
 Matches 125; Conservative 45; Mismatches 117; Indels 3; Gaps 2;
 Qy 4 VKANGITLEYEQGRHRPHPSMILLIMCGGQOLIDWPEEFIRGLAERGFRRVICEDNRDAGLS 63
 Db 125 VELGDYRLAYDSIGRSDPAIILVMGIGGQOLIDWPEEVSALEQGRVIRYDNRDGLS 184
 Qy 64 TKLEGKPNIARVFLLASNLGKPRVPYTLDDMDALDTVGMLDALGEESTHVVGVSMGMI 123
 Db 185 AWNVPPSSRLTYEVTRYRLGLPVSAVPTLTDMAIGALHLLDLD1PQAHVIGASMGMI 244
 Qy 124 AQILGAKRIGERVTSLLMTSSENPRMPAPRPOVQLKMRPKSMDEKEWIKYNLELT 183
 Db 245 AQHIAADMAPQRLLSLVLMTSGAGBGPAPSESLLILAR REAASREQAEQVQADLLAA 303
 Qy 184 IGSPGL--DREKLALDVRSKTECLCPEGTORQLAIIOSGRVRLKLRRIAVPTLVISGA 241
 Db 304 LGSPGL--DREKLALDVRSKTECLCPEGTORQLAIIOSGRVRLKLRRIAVPTLVISGA 241
 RESULT 6
 AB073253 standard; protein; 422 AA.
 XX

Db	364 ADPLLPVMIQVHVAHRSSELKLJLPGLAHRFQEAKPEPLLAAVVPPYLKA	413	ID AAW30522 standard; protein; 267 AA.
RESULT 7			
ADL05923	ADL05923 standard; protein; 360 AA.		
XX		XX	XX
AC		AC	DT 17-OCT-2003 (revised)
XX		XX	DT 26-OCT-1998 (first entry)
AC		DE	Kurthia sp. bioH gene-encoded polypeptide.
XX		XX	
DT 06-MAY-2004 (first entry)	KW Biotin; vitamin; bioH gene; Pinely CoA.	XX	
XX	Kurthia sp. 538-KA26; (DSM 10609).	OS	
DB M. catarrhialis protein #1689.	XX	OS	
XX	Moraxella catarrhialis; infection.	XX	EP853127-A2.
XX		XX	
OS	Moraxella catarrhialis.	PD	PA 15-JUL-1998.
XX		XX	PF 18-SEP-1997; 97EP-00116237.
PN US6673910-B1.		XX	PR 27-SEP-1996; 96EP-00115540.
XX		XX	(HOFF) HOFFMANN LA ROCHE & CO AG F.
PD 06-JAN-2004.	PI Furuichi Y, Hoshino T, Kimura H, Kiyasu T, Nagahashi Y;	XX	PA 1998-364652/32.
XX		XX	WPI: 1998-364652/32.
PF 04-APR-2000; 2000US-00540236.	DR N-PSDB; AAV42058.	XX	DR 1998-364652/32.
XX		XX	New DNA and vectors encoding polypeptides - used for recombinant
PR 08-APR-1999; 99US-0158416P.	PT PT production of biotin.	XX	production of biotin.
XX		XX	PS Claim 1; Page 24-25; 45pp; English.
PA (GENO-) GENOME THERAPEUTICS CORP.	CC This is a polypeptide encoded by a newly isolated bioH gene (see	XX	Claim 1; Page 24-25; 45pp; English.
XX	CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	XX	CC This is a polypeptide encoded by a newly isolated bioH gene (see
XX	CC thought to be involved in the synthesis of the biotin precursor pimelyl	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC thought to be involved in the synthesis of the biotin precursor pimelyl
XX	COA. Polypeptides (see AAV4 2058-25) encoded by novel bioH, bioA, bioP,	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	bioB, bioTII, bioHII and bioC genes (see AAV4 2054-61) of Kurthia	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	sp. are provided, as well as vectors comprising one or more of the genes,	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	CC transformed cells, and a process for the production of biotin that	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	CC comprises cultivating the transformed cells and isolating biotin from the	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	CC culture medium. Biotin is used in the preparation of pharmaceutical, food	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	CC or feed compositions. The synthesis is an improvement on prior	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	CC methods involving fermentation of e.g. E.coli and <i>Bacillus sphaericus</i> ,	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	CC which have low productivity due to accumulation of DRB, a biotin	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is	CC CC AAV4 2058) of Kurthia sp. 538-KA26 (DSM 10609). This polypeptide is
XX	CC precursor. (Updated on 17-OCT-2003 to standardise OS field)	XX	CC precursor. (Updated on 17-OCT-2003 to standardise OS field)
SQ Sequence 360 AA;	SQ Sequence 267 AA;	Query Match 32.0%; Score 481; DB 8; Length 360;	Query Match 20.8%; Score 314.5; DB 2; Length 267;
Best Local Similarity 37.3%; Pred. No 3.1e-42;	Best Local Similarity 33.1%; Pred. No 1.8e-24;	Matches 107; Conservative 61; Mismatches 111; Indels 6; Gaps 3;	Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;
Matches 6 GITELEYBGHRHPSMLIIMGQLIMGLPQVLLPBPFRGLERGRVICPDNRDAGLSPK--	QY 1 MAQVKANGITLVEBQGRHHPSMLIIMGQLIMGLPQVLLPBPFRGLERGRVICPDNRDAGLSPK--	65	QY 1 MAQVKANGITLVEBQGRHHPSMLIIMGQLIMGLPQVLLPBPFRGLERGRVICPDNRDAGLSPK--
Db 42 GIKLCEBAGGNPERPPMTITGLGSQMMWPSDQFLKRPFDAGFVIRDNRDTGLSSKIQ 101	Db 1 MPFVNHDNESLTYEV--HGQGDPPLILMGLGYNLSLW-HRTVETLAKR-FKVTFDNGV 56	122	Db 1 MPFVNHDNESLTYEV--HGQGDPPLILMGLGYNLSLW-HRTVETLAKR-FKVTFDNGV 56
QY 66 LEGYKPNLARVFLASLGMKPR--VPTLDMDALDTGLMDALGIESTHVGVSNSGGM 122	QY 121 GMIAQILGAHKGERVKSITLMITSGNPRMAPPQVLLPBPFRGLERGRVICPDNRDAGLSPK--	161	QY 121 GMIAQILGAHKGERVKSITLMITSGNPRMAPPQVLLPBPFRGLERGRVICPDNRDAGLSPK--
Db 102 IDGIPRLNTPRMKLNQAGLJSNRSBPVATLTDAEDARLKLTMQLANVNLGASNSGM 161	Db 96 GMIAQILGAHKGERVKSITLMITSGNPRMAPPQVLLPBPFRGLERGRVICPDNRDAGLSPK--	182	Db 96 GMIAQILGAHKGERVKSITLMITSGNPRMAPPQVLLPBPFRGLERGRVICPDNRDAGLSPK--
QY 123 IAQILGAKHGERVKSITLMITSGNPRMAPPQVLLPBPFRGLERGRVICPDNRDAGLSPK--	QY 124 IKYNLELITIGSPGLDREKLAQVRSIERCLCPESTORLAAILQSGSRVYKLRRIAV 233	182	QY 124 IKYNLELITIGSPGLDREKLAQVRSIERCLCPESTORLAAILQSGSRVYKLRRIAV 233
Db 162 IAQIQAARYPKYIQLVLIIFSTNSRAFLPRNPQFMTVRPESHSERDMVRHSVWFM 221	Db 156 IVYSQAFIEK-HPELJQG---DIOKRIEIITPPSAYLSQLOAQLTHDTNSN-LDKINI 208	281	Db 156 IVYSQAFIEK-HPELJQG---DIOKRIEIITPPSAYLSQLOAQLTHDTNSN-LDKINI 208
QY 183 TIGSPG-LREKLAQVRSIERCLCPESTORLAAILQSGSRVYKLRRIAVPTLVISG 241	QY 222 AVGSPGHLDIKGTRAIACERYQRNPHPLXVSQITALLASRSIRFTQIRANTLVHGN 281	281	QY 222 AVGSPGHLDIKGTRAIACERYQRNPHPLXVSQITALLASRSIRFTQIRANTLVHGN 281
Db 222 KGDIQVAPNGKQKLVAXVISARFLVGDGHDLPPVYPPLVGLISEH 328	QY 242 EDPLPILYQCGRDIAHDHIPSARFELTEGMDHIDPERHPIPLIELJAGH 288	328	QY 242 EDPLPILYQCGRDIAHDHIPSARFELTEGMDHIDPERHPIPLIELJAGH 288
QY 244 PTIVVISGAEDPLPILYQCGRDIAHDHIPSARFELTEGMDHIDPERHPIPLIELJAGH 271	Db 282 KGDIQVAPNGKQKLVAXVISARFLVGDGHDLPPVYPPLVGLISEH 328	271	QY 244 PTIVVISGAEDPLPILYQCGRDIAHDHIPSARFELTEGMDHIDPERHPIPLIELJAGH 271
Db 209 PIUJHGDAVNLYPVENGKMLAERIQQSOFHTVSCAGH 246	Db 282 KGDIQVAPNGKQKLVAXVISARFLVGDGHDLPPVYPPLVGLISEH 328	246	Db 209 PIUJHGDAVNLYPVENGKMLAERIQQSOFHTVSCAGH 246

RESULT 8
AAW30522

RESULT 11

Db	192 LSA---ADDORGEDLAGITACPRVIAFADDIVAPHLAKEDIALPEADYWHVVPDCGHYGY 248	XX	ABU21130 standard; protein; 276 AA.
Qy	272 -DITERHITPLI 282	XX	ABU21130;
Db	249 LERPDR-VNRLI 259	XX	DT 19-JUN-2003. (first entry)
			DE Protein encoded by Prokaryotic essential gene #6657.
			XX Antisense: prokaryotic essential gene, cell proliferation; drug design.
			KW Burkholderia fungorum.
			OS
			XX WO200271183-A2.
			XX PD 03-OCT-2002.
			XX PF 21-MAR-2002; 2002WO-US009107.
			XX PR 21-MAR-2001; 2001US-00815242.
			PR 06-SBP-2001; 2001US-00348992.
			PR 25-OCT-2001; 2001US-0342923P.
			PR 08-FEB-2002; 2002US-00072851.
			PR 06-MAR-2002; 2002US-03426992.
			XX PA (BLIT-) ELTRA PHARM INC.
			XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
			PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA,
			XX DR WPI: 2003-028926/02.
			XX DR N-PSDB; ACA25000.

PS SEQ ID NO 49054; 1766pp; English.

PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 49054; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*, CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of CC the target prokaryotic essential genes. Note: The sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from WIPO at CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX SQ Sequence 276 AA;

Query	3 QVKANGTILEYEEOGHRRHHPMSMLIMGGLQOLIDWPEEFIRGLAERGERFVICFCDRNDAGL 62	Score 220.5; DB 6; Length 276;
Best Local Similarity	28.6%; Pred. No. 2e-14;	Matches 84; Conservative 43; Mismatches 104; Indels 63; Gaps 12;
Matches	8 ETTRVRGOTISYBLGDPBR-TULLLHITSDASINWLST-MPAIAQRWRVIAFDQLGFGQ 65	
Db	63 STKLEGVYKPKNTARVFLASMGCLKPRTYPTLDDMALDTVGILMDALGLESTHYVGNSMGM 122	
Qy	66 SS-----KPSV-----PVPRPTLSDM-----VAPUDALGLEMVSIVGQSNKGH 104	
Db	123 IAQILGAKXHGKGEVKSLTLMITSSG--NPMPAPR-----PQVLOQEMRVPKSMDFE-- 171	
Qy	105 VAGLPAQOYPVEREAVLVNVAGYGLALPEVDPRDLGHAVTPGGL-WALNPATRDSSR 162	
Db	172 --EWIKYNELETTTSGPLDREKLALDVRKSIECPCGTQRLAAILOGCSR----- 224	
Qy	163 LIEMVFIDQGLVTEELIDGFYADRIG-----KGRGAVERSISEWARREDTL 209	
Db	225 ---VQLLRIAVPTLVISGAEIDLPLPYQCGRDIAHDHIGARFELLGGMGDIP 274	
Qy	210 ESAFTGLERR--PVNLVQARQDKVAPYHGLGRAIEGTSRFVVLVEDCGHAPP 260	
Db		

RESULT 12

AD123904	ID AD123904 standard; protein; 264 AA.
XX	XX AC AD123904;
XX	XX DT 22-APR-2004 (first entry)
XX	XX DE Streptomyces fradiae A541 locus ORF8 protein.
XX	XX KW antimicrobial; fungicide; viricide; gene therapy; lipopeptide synthesis; KW A541; NRRL 3143; antimicrobial; biosynthetic locus; ORF8.
XX	XX KW Streptomyces fradiae.
OS	XX PN US2003198981-A1.
XX	XX DR 23-OCT-2003.
XX	XX PR 24-DEC-2002; 2002US-00320079.
XX	XX PR 26-DEC-2001; 2001US-0342133P.
XX	XX PR 17-APR-2002; 2002US-137289P.
XX	XX PR 03-SEP-2002; 2002US-00232370.
PA	XX (ECOPIA BIOSCIENCES INC.
PA	XX Parnet CM, Staffa A, Zazopoulos E;
PA	XX WPI: 2003-852704/79.
PA	XX DR N-PSDB; AD123905.

PT New isolated, purified or enriched nucleic acid, useful for synthesizing PT Lipopeptides, particularly from the biosynthetic locus A54145 and NRRL PT 3143, that exhibits antimicrobial, antifungal or antiviral activity.

XX PS Claim 10; SEQ ID NO 18; 69pp; English.

The invention describes an isolated, purified or enriched nucleic acid (I) comprising: any of 4 different sequences (SEQ. ID NO: 1, 6, 17 and 34), and their coding regions; a nucleic acid having at least 75% sequence identity to a nucleic acid of (a) or complements of (a) or (b). The methods and compositions of the present invention are useful for synthesising lipopeptides, particularly A5a145 and NRL 3143, exhibiting antimicrobial, antifungal or antiviral activity. This is the amino acid sequence of the protein encoded by *Streptomyces fradiae* A5a1 biosynthetic locus ORF8.

XX Sequence 264 AA;

Query Match	14.3%	Score 216.5;	DB 7;	Length 264;
Best Local Similarity	25.8%	Pred. No. 5e-14;		
Matches 79;	Conservative	Mismatches 104;	Indels 79;	Gaps 10;
Qy	5 KANGTLEYEBCGHRRHPSMLINCLGCOLIDWPBEEFGLAERGFRYCFDNRDAGLST 64			
Db	4 RINGDLDHERRG--SGSPSLLINGSGAATGTGWLHQDALVAAGFEAWTFTR----- 55			
Qy	65 KLEGYKKPNTARVELLASMGLKPR--VPYTLDDMADLTGILMDALG1ESTHYVG 121			
Db	56 -----GTPSGGGPPTQLQDMAADTIGLIBHLGJGCAVVTGTSIGA 96			
Qy	122 MIAQILGAKGHEVYKSLLMITSSGNPRMPA-----PAPQVLQKEMR- 163			
Db	97 RVACEVARYARPDLVSRCVNMAPRARADRVTRAAATEAEI ALADSGVYVPRYAVRAMON 156			
Qy	164 -VPKSMDKEEWIKNLEL--LTIGSPGIDREKLADLVRSIERCLCPBTGTORQLAAILQ 220			
Db	157 LSPRLADDERIAWDLDFELAAGPG-----ARTQLEISAVYH 196			
Qy	221 SGSRVKKLRRIAVPLVIVSIGAEDPLPYOCGRDIAHDHPGARFELIEGMGH---DIPER 276			
Db	197 ---REEDLARITAPCRVIAFADDIVAPAHLAKEIADALEPVDGHYGYLEQFDR 253			
Qy	277 HIPRLI 282			
Db	254 -VNRLI 258			

XX Disclosure; Page 17-18; 23pp; Japanese.

New Xanthomonas maltophilia DNA sequence, useful in a method for producing 7-hydroxyindol and 7-hydroxytryptophan which are useful as raw materials for drugs, dyestuffs and reagents.

CC Disclosure; Page 17-18; 23pp; Japanese.

CC This invention relates to a *Stenotrophomonas maltophilia* (Xanthomonas maltophilia) DNA sequence which encodes 9 proteins. The invention includes CC a method for the production of 7-hydroxyindol and 7-hydroxytryptophan in CC which a microbe carrying a fragment of the DNA sequence is capable of CC hydroxylating the 7-position of indol is cultured. The DNA is useful in a CC method for producing 7-hydroxyindol and 7-hydroxytryptophan which are CC useful as raw materials for drugs, dyestuffs and reagents. The present CC sequence represents a protein encoded by the DNA of the invention

XX SQ Sequence 259 AA;

Query Match	13.9%	Score 209.5;	DB 4;	Length 259;
Best Local Similarity	28.9%	Pred. No. 2.7e-13;		
Matches 82;	Conservative	Mismatches 109;	Indels 57;	Gaps 10;
Qy	4 VKANGTLEYEBCGHRRHPSMLINCLGCOLIDW-----PEEFIRGLAERGFRYCFD 56			
Db	13 VVANGTLEYHNGH----DGAPVLMHGGPGPSAWANWRLTMB-----LATR-FVIAFD 64			
Qy	57 NRDAGLSTKLGLEYVKPKNIARVILLASNLKPRVPTYLDMDLTGVMDALG1ESTHYVG 116			
Db	65 MYGFGLYQRGPETH-----YSLDTWNQAVALLDLDIEAQASVVG 104			
Qy	117 VSNGGMIAQILGAKGHEVYKSLLMITSSGNPRMPA-----PAPQVLQKEMR 176			
Db	105 NSFGGAALALAIRHPKRVKLVLM-----GSIVGVSPFITEGLDAVNGYQPSVB----- 153			
Qy	177 NLLBLTTGSPGIDREKLADLVRSIESRCLCPBTGTORQLAAIL-----QSG-----SRVYL 227			
Db	154 NNRALDIFIA--YDRKLVUNDELAQMRYKAS10GPQESFSAMPPAPRONGVEMMASPIEQ 211			
Qy	228 LRIIAVPTLVISGAEDPLPYOCGRDIAHDHPGARFELIEGMGH 271			
Db	212 IRGIEHOTLVHGREDVPLONSYYLQATPNAQHVFHKCGH 255			

RESULT 14

ADO070988 standard; protein; 259 AA.

ID	ADO070988	standard; protein; 259 AA.
XX	XX	
AC	AC	ADO070988;
XX	XX	
DT	15-JUL-2004	(first entry)
XX	XX	
DE	DE	Stenotrophomonas maltophilia sesamol production-related protein #9.
XX	XX	
DE	DE	sesamol preparation; 1,3-benzodioxole; pharmaceutical preparation;
XX	XX	
DE	DE	antihyperensive; sesamol production-related gene cluster.
XX	XX	
OS	OS	Stenotrophomonas maltophilia.
XX	XX	
PN	PN	JP2004105064-A.
XX	XX	
PD	PD	08-APR-2004.
XX	XX	
PP	PP	18-SEP-2002; 2002JP-00271076.
XX	XX	
PR	PR	18-SEP-2002; 2002JP-00271076.
XX	XX	
PA	PA	(SAOC) MERCIAN CORP.
XX	XX	
XX	XX	DR WPI; 2004-299744/28.
PA	PA	
(SAOC) MERCIAN CORP.		N-PSDB; ADO70979.
XX	XX	Preparing sesamol, useful as raw material for pharmaceuticals, comprises PT carrying out biotransformation of 1,3-benzodioxole.
XX	XX	Disclosure; Page; 29pp; Japanese.
DR	DR	
PT	PT	The invention comprises a method for preparing sesamol, the method
XX	XX	involves using a strain of <i>Stenotrophomonas maltophilia</i> to convert 1,3-
CC	CC	-benzodioxole.

PS	PS	Raw material for pharmaceuticals, comprises
XX	XX	
PS	PS	PT carrying out biotransformation of 1,3-benzodioxole.
XX	XX	
PS	PS	Disclosure; Page; 29pp; Japanese.
XX	XX	
CC	CC	The invention comprises a method for preparing sesamol, the method
CC	CC	involves using a strain of <i>Stenotrophomonas maltophilia</i> to convert 1,3-

CC benzodioxole to sesamol. The Stenotrophomonas maltophilia bacteria
 CC contains a gene cluster (9320 nucleotide sequence given in the
 CC specification) that is involved in the conversion of 1,3-benzodioxole to
 CC sesamol. The method of the invention is useful for preparing sesamol
 CC which can be used as a synthetic raw material for pharmaceuticals such as
 CC antihypertensives. The present amino acid sequence represents a protein
 CC encoded by the Stenotrophomonas maltophilia sesamol production-related
 CC gene cluster of the invention.

XX Sequence 259 AA;

Query Match 13.9%; Score 209.5; DB 8; Length 259;
 Best Local Similarity 28.9%; Pred. No. 2.7e-13;
 Matches 82; Conservative 36; Mismatches 109; Indels 57; Gaps 10;
 Qy 4 VKGNTITLVEEQGRHHSMSLJIMGLGCQILW-----PFEFIRCLAEFGFRVTCFD 56
 Db 13 VVANGIRTYTHDAG--DGAPVLMIHGSGGGVSAWANWLTMP-----LATR-FRVIAFD 64
 Qy 57 NRDGALISTYLEGKPKPNLARVELLASMGLKPRVPTYLDDMALDTVGIMDALGIESTHVVG 116
 Db 65 MVGRGYSQRPEGIHL-----YSLDTWNQNVALIDDIEQASVVG 104
 Qy 117 VSMGGMIAICLGAHGGERVKSLLIMITSGNPNPMPQVQLKFMRVPKSMDKEEMIKY 176
 Db 105 NSFGAIALLAALAHRRPKRVKLVM----GSVGVSFPTBGLDAVWGYQPSVTS----- 153
 Qy 177 NLEBLTTTCSGPGLDREKLADLWRKSIEFLCPCGTORLAATI----QSG-----SRVKL 227
 Db 154 NMRALDIAA--YDRKLVNDELAQMRYKASIOPGFQBSFSAMPFQPPONGVEMMASPIE 211
 Qy 228 LRRTAVIPTVIISGAEDPLLPYQGRDIADHIGARFELLEGMGH 271
 Db 212 IRGIEHQTLVHVHGREDKYTPLQNSYELLQAIQNAQLHVFGKCGH 255

SQ Sequence 271 AA;
 Query Match 13.5%; Score 204; DB 5; Length 271;
 Best Local Similarity 25.0%; Pred. No. 1.e-12;
 Matches 38; Conservative 120; Mismatches 120; Indels 76; Gaps 9;
 Qy 4 VRANGTLEYEQGHHHRPHPSMLLIMMGLQDWPPEPIGLAERGRVICPDNRDRLS 63
 Db 9 VTINGPRLAYRSAGEB--PVLMIMGSAGOTWTYHOTPALHEAGYSTVYVDSR----- 61
 Qy 64 TKLEGYTKCPNTLARVFLLASMGKLPRTVPTLDDMALTQVGLMDALGIESTHVVGSMGMI 123
 Db 62 -----GPBSDV-----PAGYSLADMATDRLGLBALDIAPCRIVGTSLSGAMI 105
 Qy 124 AQILGAKHGERVKSLLIMITSSGNPNPMPAPRQ----VLQKEMRVPKSMDK----- 170
 Db 106 AQELAVDHPPELVRCVALIATLARPDDARAQNOADLLESQTVLPAYEBATAFVRMFS 165
 Qy 171 -----EWIKVNLELLTIGSGLDREKLADLWRKSIEFLCPCGTORQALALIQ 220
 Db 166 PATLNDDVAVREWLDI-FELSGTGVSAG-----GQANEL- 199
 Qy 221 SGSRVXLLRRAVPTLVISGAEDPLPYOCGRDIADHIGARFELLEGMGH---DIFER 276
 Db 200 TGDRRALRSVAPCRVISFADDLITPPHLAAEVAAIPDCDLVEISRCGHLGLYLERPDA 259
 PA (ECOP-) ECOPPA BIOSCIENCES INC.
 XX Farnet CM, Zazopoulos E, Staffa A;
 XX WPI; 2002-435445/46.
 DR N-PSDB; AAL0781.

XX Novel isolated ramoplanin biosynthetic pathway polypeptide useful for
 PT chemically modifying biological molecule that is a substrate for a
 PT polypeptide encoded by a ramoplanin biosynthesis gene cluster.

XX Search completed: April 13, 2006, 12:55:20
 Job time : 192 secs

Copyright (c) 1993 - 2006 Biocceleration Ltd.

Om protein - protein search, using sw model

Run on: April 13, 2006, 12:55:38 ; Search time 41 Seconds

(without alignments)
689.945 Million cell updates/sec

Title: US-10-686-490D-2

Perfect score: 1509

Sequence: 1 MAQVKANGITLVEEYEGHRH ERHPRLLIELIAGHAAAAAA 294

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

PIR_80;*

1: pix1;*

2: pix2;*

3: pix3;*

4: pix4;*

RESULT 1
SS7530

carboxyl esterase - Acinetobacter calcoaceticus

C.Species: Acinetobacter calcoaceticus

C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C.Accession: SS7530

R.Rok, R.G.; Barr, A.; Hellingswef, K.J.

submitted to the EMBL Data Library, June 1995

A.Description: Characterization of the estBR operon of Acinetobacter calcoaceticus BD4.

A.Reference number: SS7529

A.Accession: SS7530

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-321 <ROK>

A.Cross-references: UNIPROT:Q57172; UNIPARC:UPI00001727AA; EMBL:X68695

A.Start codon: GTG

C:Generics;

C:Superfamily: carboxyl esterase

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589.5	39.1	321	1 SS7530	carboxyl esterase
2	562.5	37.3	328	2 D83197	probable hydrolase
3	495	32.1	301	2 C70614	probable ligP prot
4	475.5	31.5	304	2 B87146	probable hydrolase
5	327.5	21.7	298	2 D95139	probable protein - Str
6	312.5	20.7	282	2 D95152	probable hydrolase
7	268.5	17.8	272	2 T36181	probable hydrolase
8	160.5	17.8	459	2 I60177	streptothricin-ace
9	234.5	15.5	265	2 A87193	probable hydrolase
10	229.5	15.2	268	2 C96028	probable 3'-oxoadip
11	228.5	15.1	262	2 E70548	probable bpcD prot
12	227.5	15.1	276	2 T30294	conserved hypothetical
13	217.5	14.4	261	2 T35708	hydrolase - Strept
14	211.5	14.0	256	2 AG3343	chloride peroxidase
15	211	14.0	262	2 S34909	carboxylesterase (
16	210	13.9	300	2 AG3214	cultivar specifici
17	200.5	13.3	393	2 B87548	hypothetical prote
18	196.5	13.0	238	2 A69463	2-hydroxy-6-oxo-6-
19	196	13.0	283	2 B38604	-poly (3-hydroxyalka
20	195	12.9	258	2 AB2770	hydrolyase (impor
21	195	12.9	261	2 C97550	hydrolyase (AJ27164
22	192	12.7	265	2 F8356	probable hydrolase
23	187	12.4	265	2 AB3115	beta-ketoacidate e
24	187	12.4	265	2 C98172	beta-ketoacidate e
25	186.5	12.4	275	2 F83243	probable hydrolase
26	184.5	12.2	647	2 C96834	unknown protein F5
27	182	12.1	263	2 C83616	beta-ketoacidate e
28	182	12.1	614	2 E9658	unknown protein, 1
29	180	11.9	285	2 S29306	poly (3-hydroxyalka

ALIGNMENTS		
Qy	6 ANGITLEYEQGHRHHPSMLIIMGQLIDMPPEPIGLABRGPRVLCFDNDAGGSTK 65	Score 589.5; DB 1; Length 321;
Db	33 SNGLELHVVEGVGNPDDEPTILLIMGLGQMLFWPDFFCKSLIDQGFGYTRFDNDRDGGSSK 92	Best Local Similarity 45.5%; Pred. No. 1.5e-41;
Qy	66 LBGV-KCPNIARVFLLASMGL-KPRVPTYLDMDALGISTHVVGVSQGMI 123	Mismatches 53; Gaps 3;
Db	93 IRHKGRRLNTKLMSRTLGLGNQAGAPYLIDMA5DVSLLAEAMRKVNVIGASQGMI 152	Indels 100;
Qy	124 AQILGAKHGERVLSLIMTISSGNPRMPAPRQVQLKRRRIAVPTLVISGA 242	Matches 130;
Db	153 AQAIAKYPEKVLALMFTSNNQPLPPPKQFLSLIGPKSSDEGIINHSKLPEI 212	Conservative
Qy	184 ICSPGCLDREKLALD-WRKSIERCLCPGTGTQRQLAAQLOGSVKLLRRIAVPTLVISGA 242	
Db	213 IGSPGVYNQVNEAIQTARKLYORSYHPAGVQVLOOFLATLCTGSNLQLDKQISQPTLVHGSR 272	
Qy	243 DPLLPYOCGRDIADHFPGARFELIENGHDIPERHLPRLLIAGH 288	
Db	273 DRLLPSHKGKAVAKGAKFELIQMGHDIPPHFIPOLSYLFKAH 318	

RESULT 2
D83197

probable hydrolase PA3586 [imported] - Pseudomonas aeruginosa (strain PAO1)
C.Species: Pseudomonas aeruginosa
C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 12-Jul-2004
C.Accession: D83197
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Li, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li;

A; Molecule type: DNA
 A; Residues: 1-298 <KUR>
 A; Cross-references: UNIPROT:054528; UNIPARC:UPI00000B37D6; GB:UJ10405; PID:9505668; PID: C; Superfamily: carboxyl esterase

Query Match Score 21.7%; DB 2; Length 298;
 Best Local Similarity 29.9%; Pred. No. 9.1e-20;
 - Matches 97; Conservative 41; Mismatches 119; Indels 67; Gaps 10;

Qy . 4 VKANGITLVEEOGHRHPPMLLNGGCOLIDPPEFRGLAERGPFTCFONRDAGS 63
 Db 6 VPSGDVELNSDDFGDPADPAILLYMGNISALGPDEPARRLADGGHLVTRIDHRDGGS 65
 Qy 64 TKELEVKKPNIARVELLASMLKLDRPVPTTLDMDALDITYGLMDALGIESTHVGVSMGEMI 123
 Db 66 T-----TRDFAAH-----PYGFELLADAVAVLDGNGVDRAHVVVLSMGATI 107

Qy 124 AQILGAKRGERVKSLTLM-----TSSGMRPMA PRPQVLOKEM---- 162
 Db 108 TQVIALDHDRLLSITMLGGGLDIDPDANIERTYMRGETLTDGPGPQ-QPPLDALALM 165

Qy 163 -----RVPKENDKEWIKYNEELLITITGSGLDREKLAIDVRKSIERCLCPEG-- 210
 Db 166 NQPAEGRALAEVARVSK-W---RILSTGTVPFDAYARVS---ERADHAGCVL 213

Qy 211 --TQRQLAIIQSGSRVKKLRRRIAVPTVYIGSAEDPLPYQCGRDIAHDIPGARFELIEG 268
 Db 214 AEPTAHYSTLTPPSRASABRETVPTVYIQAEHDPIAFAPGRKHLAGLIPTARLAEIPTG 273

Qy 269 MGHDIPERHPIRLEIAGHAAA 292
 Db 274 MGHALPSSVHGPLAEVILAHTRSA 297

RESULT 6

D9352 probable hydrolase [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA
 C; Species: Sinorhizobium meliloti
 C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C; Accession: D9352
 R; Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowes, J.; Kalman, S.; Kesting, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98: 9883-9885, 2001
 A; Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti genome. Reference number: A92622; PMID:11481432
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-282 <KUR>
 A; Cross-references: UNIPROT:092YY8; UNIPARC:UPI00000CB1A8; GB:AE006469; PID:AAK65382.1;
 A; Experimental source: Strain 1021, megaplasmid pSymA
 R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Barloy-Hubler, F.; Bowes, J.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, L.; Hyman, R.W.; Jones, T.
 Science 293: 668-672, 2001
 A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaurae, heubaut, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A; Reference number: A90339; PMID:121369234; PMID:11474104
 A; Contents: annotation
 C; Genetics:
 A; Gene: SMal127
 A; Genome: Plasmid
 C; Superfamily: carboxyl esterase

Query Match Score 20.7%; DB 2; Length 282;
 Best Local Similarity 31.3%; Pred. No. 1.5e-18;
 - Matches 93; Conservative 39; Mismatches 128; Indels 37; Gaps 7;

Qy 1 MAQVANGITLVEEOGHRHPPMLLNGGCOLIDPPEFRGLAERGPFTCFONRDAGS 60
 Db 1 MLIKGNDVIAEAFGDSAHPPVVLVQGMSMNLWWBFRCCRVAEHRGVIRYDRTD 60

RESULT 8

16071 streptothricin-acetyl-transferase - Escherichia coli
 C; Species: Escherichia coli
 C; Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C; Accession: I60717
 R; Tiepel, E.; Brevet, J.
 Plasmid 25, 217-220, 1991

A;Title: The trimethoprim resistance transposon Tn7 contains a cryptic streptothricin resistance number: 16017; MUID:92021239; PMID:1656477	Db	156 LNDVYAVADWIAFMNWPDKS--TPGL-----RC----PQN 190
A;Accession: 16017	Qy	223 SRYKLRLRRAVPTLVISGAEDPLPQQGRDIADHIGARFELIEGMGH---DIPERHI 278
A;Status: preliminary; translated from GB/EMBL/DBJ	Db	191 NRLPAYRSTAAPVIGFAEDVTPPSLGREVAEVLPNGRLQIPDAGLGFPERPEAVN 250
A;Molecule type: DNA		
A;Residues: 1-459 <RES>		
A;Cross-references: UNIPROT:Q47625; UNIPARC:UPI00000AF08C; EMBL:X56815; NID:9499063; PMID:1499883	Qy	279 PRLELIG 287
C;SuperFamily: streptothricin acetyltransferase	Db	251 AAUQFFAG 259
Query Match Score 17.8%; DB 2; Length 459;		
Best Local Similarity 29.6%; Pred. No. 1.3e-14;		
Matches 86; Conservative 56; Mismatches 108; Indels 41; Gaps 13;		
3 QVKANGTLEYEEQGHRRHPSMLLIMLGQLIDMPPEEFIRGLAERGFRVICFDNRDAGL 62		RESULT 10
Db 20 KVVRRAISLTESFGDPAHPIIILM-AMSAVWPDEFPSQLXKMRVTRDHR-AGK 77		C96028
Qy 63 STKLEGVKPNIARYVLLASMGKPRVPXTLDDWALDTVGMDALGIESTHVVYGSMGCM 122		probable 3'-oxoadipate enol-lactonase (EC 3.1.1.24) [imported] - Sinorhizobium meliloti
Db 78 STSYE-----PCQAPSVEELA-DDVTRVDGXGLEAHLVCMSLGGF 118		C;Species: Sinorhizobium meliloti
Qy 123 IAQIUGKAGGERVSLTLMIT--SSGNPMPMAPPPQVQKMRVPKS--MDKEEWIKY 177		C;Accession: C96028
Db 119 LSQLV-ALNPKVSLTLEKQHAESELWDSDRNDAVVAQ 176		Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
Qy 178 LELLTIGTSP-GLDREKLALDVRSKIERCLCPEGFTQRLAAIQLS--GSRVQLLRRI-A 232		R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hern.
Db 177 VAWRNSGTAHAFDEKIQNIAQNLNFD-----PNNLTTFNHTLGGGERWGRNLNET 229		Proc. Natl. Acad. Sci. U.S.A. 98, 9839-9844, 2001
Qy 233 VPTLVISGAEDPLPQQGRDIADHIGARFELIEGMGHIDPERHIPRLIE 283		A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing em
Db 230 VPTLHGTEDPVLPVHGLAKE-ARGSKMLTLEGTHGBLHHEDWPRTIQ 279		A;Reference number: A95842; MUID:21396508; PMID:11481431
RESULT 9		A;Status: preliminary
A87193 probable hydrolase [imported] - Mycobacterium leprae		A;Molecule type: DNA
C;Species: Mycobacterium leprae		A;Residues: 1-268 <KUR>
C;Accession: A87193		A;Cross-references: UNIPROT:UPI00000CB8A6; GB:AL591985; PIDN:CA49891.
R;Cole, S.T.; Bigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Houlden, M.A.; Rutherford, K.M.		A;Experimental source: strain 1001, megaplasmid pSymB
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, J.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.;		R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubelle, D.; Chain, P.; Cowie, A.; Dreano, S.; Fedderspiel, N.A.; Fisher, R.F.; Hyman, R.W.; Jones, T.
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.;		Science 293, 668-672, 2001
A;Title: Massive gene decay in the leprosy bacillus.		A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Kompa, C.; Leelaar, hebuilt, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, J.
A;Reference number: A86909; MUID:21128732; PMID:11234002		A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Status: preliminary		A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Molecule type: DNA		A;Content:
A;Residues: 1-265 <STO>		A;Genes: pcad; SB20579
A;Cross-references: UNIPROT:Q9CB11; UNIPARC:UPI000006E55; GB:AL450380; NID:913033907; F		A;Gene: plasmid
C;Genetics:		C;Superfamily: carboxyl esterase
C;Genetics:		C;Keywords: carboxyl ester hydrolase
Query Match Score 15.5%; DB 2; Length 265;		Query Match Score 229.5%; DB 2; Length 268;
Best Local Similarity 26.9%; Pred. No. 4.4e-12;		Best Local Similarity 27.2%; Pred. No. 1.2e-11;
Matches 83; Conservative 41; Mismatches 104; Indels 81; Gaps 12;		Mismatches 95; Indels 79; Gaps 10;
9 ITLEYEEQGHRRHPSMLLIMLGQLIDMPPEEFIRGLAERGFRVICFDNRDAGLSTKLEG 68	Qy	1 MAQYKANTITLEEQQGH-RHHPMSMLIIMGQQLIDMPPEEFIRGLAERGFRVICFDNRD 59
2 INLAVEDRGTE--PVVFAGRGGRGTRTOPOHAFLAGYRITFDORGIGATENTG 59	Db	1 MQPTRINDVTIHYRVGAVTEKPALVFLINSLGDFRIMDRVVFLRLAGD--FAIVLYDKRG 58
69 VPKPNIARYVLLASMGKPRVPXTLDDWALDTVGMDALGIESTHVVYGSMGMAQILG 128	Qy	60 AGJSTKLEGVKKPNIARYVLLASMGKPRVPXTLDDWALDTVGMDALGIESTHVVYGS 119
60 -----PITQTQVADTAVLIESGAVPARIVGYSMGSFIQAELM 97	Db	59 HGUS-----DIG--QVPSIESHDATDLAGLDRLLAVQAIQVGLSV 97
120 GGMIAQILGAKIGERVKSLTLMITSGNPRMPPQVLOKEMRPKSMDKEEWIKYNE 179	Qy	120 GGMIAQILGAKIGERVKSLTLMITSGNPRMPPQVLOKEMRPKSMDKEEWIKYNE 179
Db 98 GJIAQS1YGRPEPDLYRALVLSGTA-----HKIGTVEFWDA 133		Db 98 GJIAQS1YGRPEPDLYRALVLSGTA-----HKIGTVEFWDA 133
Qy 180 LUTTIGSGLDRKLDLAVRKTSIERCLCPEGTQRLLAQSGSRVLLR-----229		Qy 180 LUTTIGSGLDRKLDLAVRKTSIERCLCPEGTQRLLAQSGSRVLLR-----229
Db 134 RTRAEAHGI--EAVADGV--LERWFTPAFRPENLAF--TGYRNMVRQPVPGYVGTC 186		Db 134 RTRAEAHGI--EAVADGV--LERWFTPAFRPENLAF--TGYRNMVRQPVPGYVGTC 186
Qy 230 -----RIVAEPTLVISGAEPPLPQCGRGTADHIFGARFELIEGMGHID 274		Qy 230 -----RIVAEPTLVISGAEPPLPQCGRGTADHIFGARFELIEGMGHID 274
Db 187 AAIRADTDEAAGRIVAVPLVLCVGDQGSTPBDLVRSTADLIFGARPEVIRGAGH-IP 243		Db 187 AAIRADTDEAAGRIVAVPLVLCVGDQGSTPBDLVRSTADLIFGARPEVIRGAGH-IP 243
RESULT 11		
E07048		
98 VARPSLVRAVLMAVRGRDLRTRQFFHAEAEBFDGQIOLPSGYNAYKVRLENUSR--KT 155		
C;Species: Mycobacterium tuberculosis		
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004		
168 MDKE --- EWI-KYNLELLTTIGSPLDREKLADVRSKIERCLCPGTQRQLAAILQS 222		

A;Molecule type: DNA
 A;Residues: 1-256 <KUR>
 A;Cross-references: UNIPROT:08193 ; UNIPARC:UPI0000057DC7 ; GB:AE008917 ; PIDN:AAL51914.1 ;
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BME10733
 A;Map position: I
 C;Superfamily: tropinesterase
 C;Keywords: oxidoreductase

Query Match 14.0%; Score 211.5; DB 2; Length 256;
 Best Local Similarity 28.2%; Pred. No. 3.5e-10; Indels 91; Gaps 12;
 Matches 82; Conservative 27; Mismatches 91;

Qy 7 NGITLFEYEQHRHPSMILIMGL-GGQJIDWPSE-FVGLAERGERVICEDNBDAGLST 64
 Db 12 DGLRLAYRQAG--EGDPILLIHGFASSSLVNPSPGMWFTLTEGYRVIAIDNRGRGFST 69
 Qy 65 KLEGIVYKPNIARVFLIASMLKPRVPTDLMALDTVGWMDAIGIESTHVGYSMGMINA 124
 Db 70 KSHKAE-----DTYPSKWMRDAALDHLGIAKHWGYSMGARIS 110
 Qy 125 QILGAKRHGERVKSLTL-----MITSSGN-----PRMPA----PRPOVLOQKFRVP 165
 Db 111 AVLAIEHSSEVRHSAVFGGGIGMVIGAGWPIGEALLMEDPATITHPGQMFRFADQT 170
 Qy 166 KSMDFKEEWKXNLLELTIGSPGLDREKALDVKSIERCLCPFGTQRQAAFLQSRSV 225
 Db 171 RS-----DRIAAACVITSKE-LVP-----V 190
 Qy 226 KLLRIIAVPTLVISGAEDPLLPYQCGRDADHPIGARFFLIEGMHDPER 276
 Db 191 AAIEPILQPVIVAVGTTDDIA-QSAQELANLIP-----NGEALDIPGR 232

Search completed: April 13, 2006, 13:00:03
 Job time : 42 secs

Query Match 23.1%; Score 211.5; DB 2; Length 256;
 Best Local Similarity 28.1%; Pred. No. 3.5e-10; Indels 91; Gaps 12;
 Matches 82; Conservative 27; Mismatches 91;

Db 201 INAKTHYIWASEDKIVTKDQQRMVLVNGISGAKETCIBESGHFPDMEADBEFI 252

Search completed: April 13, 2006, 13:00:03
 Job time : 42 secs

RESULT 15
 S34609 carboxylesterase (EC 3.1.1.1) - Pseudomonas sp. (strain KWI-56)
 C;Species: Pseudomonas sp.
 A;Variety: strain KWI-56
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 12-Jul-2004
 C;Accession: S34609
 R;Shimada, Y.; Nagao, T.; Sugihara, A.; Iizumi, T.; Fukase, T.;
 Biophys. Acta 1174, 79-82, 1993
 A;Title: Cloning and sequence analysis of an esterase gene from Pseudomonas sp. KWI-56.
 A;Reference number: S34609 ; MUID:193326640 ; PMID:8334166
 A;Accession: S34609
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-262 <SH1>
 A;Cross-references: UNIPROT:09ZUB ; UNIPARC:UPI00000B7399 ; GB:D14529 ; NID:9197834 ; PIDN:
 C;Superfamily: tropinesterase
 C;Keywords: carboxylic ester hydrolase

Query Match 14.0%; Score 211; DB 2; Length 262;
 Best Local Similarity 26.4%; Pred. No. 4e-10; Indels 64; Gaps 9;
 Matches 77; Conservative 44; Mismatches 107;

Qy 7 NG-ITLFEYEQHRHPSMILIMGL-GQJIDWPSE-FVGLAERGERVICEDNBDAGLST 65
 Db 5 NGNVNLSDYDVAGHGB--CFFIAGTAGSDSMW--DGLRDELSKGRTYAFDNRDGESTI 60
 Qy 66 LEGYKKPNIARVFLIASMLKPRVPTDLMALDTVGWMDAIGIESTHVGYSMGMINA 125
 Db 61 CD-----QYTMQLDALKDALSYMDAEGLQKAIHGSLGNTIAQ 99
 Qy 126 ILGAKHGERVKSLTIMITSGNPNPAPPAFPQVLOKEMPKNSNDKEEKVYNLELTIG 185
 Db 100 ELLAIAPDVSITLNUVNTS--RDNVMSVIELARDWSKUTDORUINRSYFL--- 152
 Qy 186 SPGLDREKALDVKRSKTSRCLCPGTQRQAAFLQGSVSKLRR----- 230
 Db 153 --ALGSKALGSDIFNQVV-----DFAASGSQSOPREALIRQWEIDLTVDTTDRLSL 200

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.
 protein - protein search, using sw model
 on on: April 13, 2006, 12:52:23 ; Search time 231 Seconds
 (without alignments)
 897.945 Million cell updates/sec
 title: US-10-686-490D-2
 reflect score: 1509
 influence: 1
 MACRURANICIN PYROPOUCH
 RPHDPFLYIYIACHAIIAFAA 294

Digitized by srujanika@gmail.com

Gapop 10.0 , Gapext 0.5

searched: 2166443 seqs, 705528306 residues

[๑๖]

length: 9
length: 800000000

March 66

Maximum Match 100%

LISTING FIFTEEN OF BIBLICAL REFERENCES

database : UniProt_05.80:*

*uninfect trembl : **

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. This is derived by analysis of the total score distribution.

תומאס

Query built	Score No.	Match	Length	DB	ID	Description	
						Q4tr38_9SPIN	Q4tr38 erythrobact
1	689	45.7	296	2	Q4TR38_9SPIN	Q9kiu0 uncultured	Q9kiu0 uncultured
2	623.5	41.3	438	2	Q9KIU0_9BACT	Q79q78 acinetobact	Q79q78 acinetobact
3	589.5	39.1	312	2	Q79A78_ACICA	Q57172 acinetobact	Q57172 acinetobact
4	589	39.1	312	2	Q57172_ACIAD	Q6d508 erwinia car	Q6d508 erwinia car
5	579	38.4	306	2	Q6D508_ERWCT	Q9hv40 pseudomonas	Q9hv40 pseudomonas
6	562.5	37.3	328	2	Q9HY40_PSEAE	Q8849y pseudomonas	Q8849y pseudomonas
7	562.5	37.3	378	2	Q8849y_PSEPK	Q4k713 pseudomonas	Q4k713 pseudomonas
8	561.5	37.2	397	2	Q4K713_PSEPKS	Q97tk4 clostridium	Q97tk4 clostridium
9	556.5	36.9	299	2	Q97TK4_CLOAB	Q8978y bradyrhizob	Q8978y bradyrhizob
10	552	36.6	304	2	Q8978y_BRAJA	Q87XKO_PSEBM	Q87XKO_PSEBM
11	548.5	36.3	330	2	Q87XKO_PSEBM	Q4E596 psychrobact	Q4E596 psychrobact
12	542	35.9	345	2	Q4FSG6_9GAMM	Q4ZPH7 pseudomonas	Q4ZPH7 pseudomonas
13	540	35.8	330	2	Q4ZPH7_PSESY	Q4J684 azotobacter	Q4J684 azotobacter
14	536.5	35.6	328	2	Q4J684_AZOVI	Q582C7 trypanosoma	Q582C7 trypanosoma
15	488	32.3	312	2	P9682C7_9TRYP	P969335 mycobacteri	P969335 mycobacteri
16	485	32.1	301	2	P969335_MYCTU	Q7uij8 mycobacteri	Q7uij8 mycobacteri
17	485	32.1	301	2	Q7UIJ8_MYCB	Q7dh96 MYCTU	Q7dh96 MYCTU
18	485	32.1	336	2	Q7DH96_MYCTU	Q9cbk5 mycobacteri	Q9cbk5 mycobacteri
19	475.5	31.5	304	2	Q9CBK5_MYCPA	Q73sf6 leishmania	Q73sf6 leishmania
20	474.5	31.4	302	2	Q73SF6_MYCPA	Q8845_pseudomonas	Q8845_pseudomonas
21	473.5	31.4	291	2	Q8845_PSEPK	Q51v17 billiibacte	Q51v17 billiibacte
22	473	31.1	291	2	Q51V17_PSILPO	Q5md37 cystobacter	Q5md37 cystobacter
23	426.5	28.3	298	2	Q5MD37_9DELT	Q9apw4 pseudomonas	Q9apw4 pseudomonas
24	425.5	28.2	291	2	Q9APW4_PSEAE	Q4qba8 leishmania	Q4qba8 leishmania
25	425	28.2	346	2	Q4QBA8_LEIMA	Q4q885 leishmania	Q4q885 leishmania
26	378	25.0	716	2	Q4QB85_LEIMA	Q75qp7 escherichia	Q75qp7 escherichia
27	376	24.9	280	2	Q75QP7_ECOLI	Q4qe87 leishmania	Q4qe87 leishmania
28	375.5	24.9	432	2	Q4QE87_LEIMA	Q56Q28 escherichia	Q56Q28 escherichia
29	372	24.7	280	2	Q56Q28_ECOLI	Q75Q00 salmonella	Q75Q00 salmonella
30	372	24.5	280	2	Q75Q00_SALLEN	Q75WMP1 escherichia	Q75WMP1 escherichia

RESULT 1

Q4TR8 9SPHN	PRELIMINARY;	PRT;
ID Q4TR8_9SPHN		296 AA.
AC Q4TR8;		
DT 13-SEP-2005	(TREMBLrel. 31, Created)	
DT 13-SEP-2005	(TREMBLrel. 31, Last sequence update)	
DT 13-SEP-2005	(TREMBLrel. 31, Last annotation update)	
DE Probable hydrolase.		
DN ORFNames=ELIO088;		
OS Erythrobacter litoralis HTCC2594.		
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;		
OC Sphingomonadaceae; Erythrobacter.		

Query Match	45.7%	Score 689;	DB 2;	Length 296;
Best Local Similarity	45.4%	Pred. No. 2e-44;		
Matches	133;	Conservative	59;	Mismatches 99; Indels 2; Gaps 1;
Qy	1 MAOYKANGITLLEYEQGHRHPSMLLNGGGQLIDWPBBSFTIRGLAERGFRRVICFDNRDA 60			
Db	1 MPEFTANGTIIHYDHGPDAEPLLINGFAONTLWPMBLVEALTHGPFRTRNHDIVD 60			
Qy	61 GLSPTKLEGVYKPNIAVRYFLASAMCLKPRVPTYLDDMALTDTVGLMDALGTESTHVGSMG 120			
Db	61 GLSQRPDGTAQPGJLKTLGKLGFTPKVPTYLADMAODSAGVLDALGIGOAHVGGSMG 120			
Qy	121 GMIAQIQLGAKHGERVKSLTMLMTSSGNPMPMAPRQPVQKFMVRPKSDKEENIKYNEEL 180			
Db	121 GMIAQHVAARHPDKTKLTSIFSTTGKLPPAKKEAQTLTRPKSLEEVLVEHGJKL 180			
Qy	181 LTTIGSPG - LDREKLAALDVRKSTERCILCPEGFTQRQLAILQGSRSRVLRLRAVPTLVYI 238			
Db	181 SRAIGSPGYPAEERLREFEVREGTRSYPEGPTRHLSAIVAOGDRREMPLKSITAPTLVL 240			
Qy	239 SGABDPPLPYOCGRDIAHDPGARFELIEGMGDHIPRHLIELJELAGHAA 291			

RESULT 2 09KIUQ 9BACT

RT oxR.;"	DR EMBL; BX950851; CAG75135.1; -; Genomic_DNA.
RL J. Bacteriol. 181:2925-2928 (1999).	DR GO; GO-0016787; F:hydrolase activity; IEA.
[5]	DR InterPro; IPR000073; A/b_hydrolyse.
NC_001514110; DOI=10.1093/nar/gkh910;	DR Pfam; PF00561; Abhydrolase_1.
RX Pubmed=15263089; DOI=10.1073/pnas.0402424101;	KW Complete proteome; Hydrolase.
RA Barbe V., Valenet D., Ponknecht N., Kreimeyer A., Oztas S.,	SEQUENCE 306 AA; 33739 MW; SA0F2613FBEB5B2 CRC64;
RA Labarre L., Cruvelier S., Robert P., Duprat S., Wincker B.,	Query Match 38.4%; Score 579; DB 2; Length 306;
RA Ornston L.N., Weissbach J., Mariere P., Cohen G.N., Medigue C.;	Best Local Similarity 43.9%; Pred. No. 5..3e-36;
RT "Unique features revealed by the genome sequence of Acinetobacter sp. ADP1, a versatile and natural transformation competent bacterium.,"	Mismatches 45;保守性 105; Indels 6; Gaps 3;
RT Nucleic Acids Res. 32:5766-5779 (2004).	Matches 122; Conservative 45; Mismatches 45; Indels 6; Gaps 3;
RL Nucleic Acids Res. 32:5766-5779 (2004).	Qy 4 VRANGITLVEEGQRHPSMLLIMGGQLIDWPPEFIRGLAERGPRVICFDNRDAGLS 63
DR EMBL; ZA8863; CAAB8927.1.; -; Genomic_DNA.	Db 5 IRNKGNVIAYESGDESTEEILVLAGLSQSMISWSDAQCOTVSRSGYVIREDFRDVGCS 64
DR PIR; S57530; S57530.	64 TKLEGVKKPNIARVFLASMGKLPKRVPTYLDMDALTVGLMDALGTESTHVVGSMMGI 123
DR PIR; S57530; S57530.	65 SHYDSPVNPNGVNKAISANRPDPVSTDDAGDLIGMDALISIAAHFTVGRSGMGI 124
DR GO; GO:0016787; F:hydrolase activity; IEA.	SEQUENCE 312 AA; 34681 MW; 14E020BA7654D905 CRC64;
DR InterPro; IPR000073; A/b_hydrolyse.	Query Match 39.1%; Score 58.5%; DB 2; Length 312;
DR InterPro; IPR000379; Ser estrs.	Best Local Similarity 45.5%; Pred. No. 8..6e-37; Mismatches 53; Conservatve 53; Indels 3; Gaps 3;
DR Pfam; PF00561; Abhydrolase_1; 1.	Db 125 AQIQAARIPIPERVTLSSLTIMSSSNPSLPQTADPM_ALMTOPPNPFLNEPEYLNHLRL 183
Complete proteome; Hydrolase.	Db 126 AERLAKTYPDTERTYRSQKEELRCEFNPEGFTRQNALVASGDRRKLLATIAAPTLV 238
SEQUENCE 312 AA;	Db 127 AQLGAKHGERVSLTMITSSNPNRMPAPRPPQVLOKMRVPKS_--_MDKEEWIKXNUEL 180
Query Match 39.1%; Score 58.5%; DB 2; Length 312;	Qy 6 ANGITLEYERQGRHRPHPSMLLIMGGQLIDWPPEFIRGLAERGPRVICFDNRDAGLS 65
Best Local Similarity 45.5%; Pred. No. 8..6e-37; Mismatches 53; Conservatve 53; Indels 3; Gaps 3;	Db 128 SNGIBLHVYGGNPDPHTILLIMGLGAQNLFWPDFFCKSLIDQGYVTFNDRDIGLSK 83
Db 24 SNGIBLHVYGGNPDPHTILLIMGLGAQNLFWPDFFCKSLIDQGYVTFNDRDIGLSK	Db 129 SGAEDPLPYQCGGRDIADHPIGARFELIEGMGHIDIPER 276
Qy 66 LEGV_KKPNIARVFLASGCL_-KRPVPTLDDMDALTVGLMDALGTESTHVVGSMMGI 123	Db 130 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 238
Db 84 TRHKSKKRNLTKLMSRFTGLGNQCAPTYLDMAEDVSILTEAMRIRKVNIVGASMGMGI 143	Db 131 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 243
Qy 124 AQLGAKHGERVSLTMITSSNPNRMPAPRPPQVLOKMRVPKS_--_MDKEEWIKXNUEL 183	Db 132 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 243
Db 144 AQIQAARIPIPERVTLSSLTIMSSSNPSLPQTADPM_ALMTOPPNPFLNEPEYLNHLRL 183	Db 133 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 243
Db 144 AQIQAARIPIPERVTLSSLTIMSSSNPSLPQTADPM_ALMTOPPNPFLNEPEYLNHLRL 183	Db 134 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 243
Qy 184 IGSPLGLDRBKLAUD_VKSTERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLVISGA 242	Db 135 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 243
Db 204 IGSPLGPyVNVEAIQPKYIQRSTHPAGLQQFIALCQLQDKQISQPTLVISGR 263	Db 136 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 243
Qy 243 DPLPYQCGGRDIADHPIGARFELIEGMGHIDIPER 288	Db 137 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 243
Db 264 DRJLPPSHSKAVAKAIKGAKFELIQGMGHDIPPHFIPOLSYLFHH 309	Db 138 TTTGSP_-GLDEBKLAUDVRSKIERCLCPGTQRQLAAILOGGSRSVLLRRIAVPTLV 243
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	RESULT 6
OC Pseudomonadaceae; Pseudomonas.	QSYH40_PSEAE
OC NCBItaxonID=287;	ID QSYH40_PSEAE PRELIMINARY;
OX RN [1]	PRT; 328 AA.
RN NUCLEOTIDE SEQUENCE [1]	DB 139
RP STRAIN=ATCC 15692 / PA01;	DR EMBL; AE004779; AAG06974..1; -; Genomic_DNA.
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	DR PIR; DB3197; DB3197.
AC 06D508;"	DR GO; GO-0016787; F:hydrolase activity; IEA.
DT 25-OCT-2004 (TREMBLrel. 28, Created)	DR InterPro; IPR000073; A/b_hydrolyse.
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)	DR InterPro; IPR000379; Ser estrs.
DB Probable hydrolase.	DR Pfam; PF00561; Abhydrolase_1.
OS OrdredLocusName=CA2233;	KW Complete proteome; Hydrolase.
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	SEQUENCE 328 AA; 35604 MW; C3DDA69157505F77 CRC64;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Query Match 37.3%; Score 562.5; DB 2; Length 328;
OC Enterobacteriaceae; Pectobacterium.	Best Local Similarity 43.1%; Pred. No. 1..1e-34; Mismatches 117; Indels 3; Gaps 2;
OX NCBI_TaxID=23471;	RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT carotovora subsp. atroseptica and characterization of virulence
AC 06D508;"	RT factors";
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)	RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT
OS OrdredLocusName=CA2233;	RT
OS Brevibacter carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).	RT
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	RT
OC Enterobacteriaceae; Pectobacterium.	RT
OX NCBI_TaxID=23471;	RT
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	RT
RC SPRAIN=ICRI 1043 / ATCC BAA-672;	RT
AC 06D508;"	RT
DT 25-OCT-2004 (TREMBLrel. 28, Created)	RT
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)	RT
DB Probable hydrolase.	RT

Qy	4 VRANGITLEYEBOQHRRHPSMILLIGQLIDWPPEFTIRGLAERGFRVTCFDNRDAGL 63	Db	198 IAQHLAAAMPERTSLLTVMSSSGAAGLPAPDPALVQOLLAR-RSAPNREVAEQADILLA 256
Db	31 VELGDYRLLAQSIGRSDPALLVWLGQJHWPPEVALCEQFRTYFDNRDVLG 90	Qy	183 TIGSPGL--DREKLALDVRKSIRCLCPEGTOROLAATLQSRSRVKLLRRIAVPTLVISG 240
Qy	64 TKLEGVKPKNTARYFLAASMGUKPRVPTYLDDMALTIVGMDALGIESTHVGYSMGCGI 123	Db	257 ALGSPEVRDDEREVLLHQAAQAYDRAFNPGAKQIMATAEPSRVELLNOLRVETLVVHG 316
Db	91 AWNVPPSRTSYEVYRLPVSAPPYLTDMAGDHLLDIPQAHVLGASMGGNI 150	Qy	241 AEDPLPTOCGRDIADH1PGARFELIEGMGHDIPE 275
Qy	124 AQILGAHKGERVKSLLIMITSSGPNRMAPPQVLOKFRVPSKMDKEWEIKYNNELLTT 183	Db	317 TADPLPVNHGVHLAAHTRSQURLPGLAHRFQE 351
Db	151 AQHIADMAPORLSSLTVMTSSGAEGLPASESLLRAR-REASREGAVEQADILLA 209	Qy	RESULT 8
Qy	184 IGSPLGL--DREKLALDVRKSIRCLCPEGTOROLAALQGSRSRVKLLRRIAVPTLVISG 241	Db	Q4K713_PSEF5
Db	210 IGSPLPVDRDQOLLAQSRDRAINPPEGVQQLLALPEPSRFLPLNLQVPTIVRG 269	Qy	ID Q4K713_PSEFS PRELIMINARY; PRT; 397 AA.
AC	Q8BNY9_PSEPK PRELIMINARY;	Db	AC Q4K713_PSEFS PRELIMINARY;
DT	01-JUN-2003 (TREMBLrel. 24, Created)	Qy	AC Q4K713_PSEFS PRELIMINARY;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)	Db	AC Q4K713_PSEFS PRELIMINARY;
DN	Hydrolease, alpha/beta fold family.	Qy	DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
GN	OrderedLocusName=pp1064;	Db	DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
OS	Pseudomonas putida (strain K72440).	Qy	DE Hydrolyase, alpha/beta fold family.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	Db	DE Hydrolase, alpha/beta fold family.
OX	Pseudomonadaceae; Pseudomonas.	Qy	GN ORPName=PF1_4889;
NCBI_TAXID=160488;	RN Pseudomonas fluorescens (strain PF-5).	Db	GN Pseudomonas fluorescens (strain PF-5).
RP	NUCLEOTIDE SEQUENCE,	Qy	OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
RX	MBDLINEB=2423060; PubMed=125234463;	Db	OC Pseudomonas.
RX	DOI=10.1046/j.1462-2942.2002.00366.x;	Qy	NCBI_TAXID=20664;
RA	Martin K.E., Weinert C., Paulsen T.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.B., Gill S.R., Pop M., Holmes M., Brinkac M.J., Beaman M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K., Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Weder H., Tauber J., Stjepanic D., Roheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B., Fraser C.M., "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.", EMBL; AR016778; AN66689.1; -; Genomic_DNA.	Db	NCBI_TAXID=20664;
RA	TIGR; PP1064; -; Genomic_DNA.	Qy	RT 9 ITLEYEEOGRHRPHPSMILLIGQLIDWPPEFTIRGLAERGFRVICFDNRDAGL 68
DR	GO:0016787; F:hydrolyase activity; IEA.	Db	RT 94 VSLAYQSTGRTSDDPALLVMGLGGQLIHWDEVVVQGPGRVIRYDNRDGLSTVROA 153
DR	GO:0016740; F:transferase activity; IEA.	Qy	RT 69 VKKPNIAVFLASMGKLPVRPYTLDMDALDVTGLMAGLISSTHVVGSMGMAQILG 128
RT	InterPro; IPR000073; A/B_hydrolease.	Db	RT 154 PYSANLTFEVLRYKLGPVAAYTLTMDADDGLMDALH1QFHVLGASMGMAQHLA 213
RT	InterPro; IPR000073; Ser esterase.	Qy	RT 129 AKHGERYKSLTLMITSSGPNRMAPPQVLOKFRVPSKSMDKEWIKYNLLETTIGSPG 188
DR	Pfam; PF0561; Abhydrolase_1.	Db	RT 214 AMEPRVYESLTLIMTSSGAEGLPAPNALVQLSR-RNAPSREAALBQADLLAALGSPK 272
KW	Complete proteome; Hydrolase; Sequence	Qy	RT 189 L--DREKLALDVRKSIRCLCPEGTOROLAATLQSRSRVKLLRRIAVPTLVISGAEDPL 246
Qy	3 VRANGITLEYEBOQHRRHPSMILLIGQLIDWPPEFTIRGLAERGFRVICFDNRDAGL 62	Db	RT 273 VSDDRQVLLQQAAVAVYRAFNPSEGVRQIMATAEPSRVALLQQLRVTLVHGTADPL 332
Qy	7 Test Local Similarity 37.3%; Score 562.5; DB 2; Length 378; Matches 122; Conservative 44.4%; Pred. No. 1.3e-34; Indels 3; Gaps 2;	Qy	RESULT 9
Db	78 RAELGAVSLVYQSVSAPRDBALLVMGLGGQLIHWPDDEAELCROGFVIRYDNRDVLG 137	Qy	Q97TK4_CLOAB PRELIMINARY; PRT; 299 AA.
Qy	63 STKLEGVKPKNTARYFLAASMGUKPRVPTYLDDMALTIVGMDALGIESTHVGYSMGCG 122	Db	Q97TK4_CLOAB PRELIMINARY; PRT; 299 AA.
Db	138 SRMNQVPPHANLTLLRKLGPVSAPPFTLTDADDGHLHMDALGVRQFHVLGVSNCM 197	Qy	AC Q97TK4_CLOAB PRELIMINARY; PRT; 299 AA.
Qy	123 IAQILGAHKGERVKSLLMITSSGPNRMAPPQVLOKFRVPSKSMDKEWIKYNLLETTIGSPG 182	Db	AC Q97TK4_CLOAB PRELIMINARY; PRT; 299 AA.

Qy	239	SGAEDPLLYQCGRDIAHDHIPGARFELLEGGMGHDIPE	275		Db	215	VEVDREQLRQDATAIDRAFNPEGVKGQILAVLAEPSEVLLHULPTLVHGTADPL	274
Db	267	HGTADPLLFYMGHGTVRAHIIQGSQRLPGLAHRFQS	303		Qy	247	PYQCGRDIAHDHIPGARFELLEGGMGHDIPE	275
RESULT 14								
Q4J684	AZ0VI	PRELIMINARY;	PRT;	328 AA.				
AC	Q4J684;							
DT	13-SEP-2005	(TREMBLrel. 31, Created)						
DT	13-SEP-2005	(TREMBLrel. 31, Last sequence update)						
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)						
DE	Alpha/beta hydrolase fold precursor.							
GN	ORFName=AvINDRAFT_8586;							
OS	Azotobacter vinelandii AvOp							
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;							
OC	Pseudomonadaceae; Azotobacter.							
OX	NCBI_TaxID=32271;							
RN	[1]							
RP	NUCLEOTIDE SEQUENCE.							
RC	STRAIN=AVOp;							
RG	US DOB Joint Genome Institute (JGI-PGP);							
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,							
RA	Hammon N., Israeni S., Pitluck S., Richardson P.;							
RA	"Sequencing of the draft genome assembly of Azotobacter vinelandii AvOp."							
RT	Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.							
RL	[2]							
RN	NUCLEOTIDE SEQUENCE.							
RC	STRAIN=AVOp;							
RG	US DOB Joint Genome Institute (JGI-ORNL);							
RA	Ramer F., Land M.;							
RA	"Annotation of the draft genome assembly of Azotobacter vinelandii AvOp."							
RT	Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.							
RL	[3]							
RN	NUCLEOTIDE SEQUENCE.							
RC	STRAIN=AVOp;							
RG	US DOB Joint Genome Institute (JGI-ORNL);							
RA	Larimer F., Land M.;							
RA	"Annotation of the draft genome assembly of Azotobacter vinelandii AvOp."							
RT	Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.							
RL	[4]							
RN	NUCLEOTIDE SEQUENCE.							
RC	STRAIN=AVOp;							
RG	US DOB Joint Genome Institute (JGI-PGP);							
RA	Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,							
RA	Hammon N., Israeni S., Pitluck S., Richardson P.;							
RA	Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.							
CC	-1- CAUTION: The sequence shown here is derived from an							
CC	ENMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is							
CC	preliminary data.							
DR	EMLB: AAAU0000001; EAM06907-1; -; Genomic_DNA.							
KW	Hydrolease; Signal.							
FT	SIGNAL;	32	Potential					
SQ	SEQUENCE 328 AA; 36068 MW;	3258374E36CC4A7D	CRC64;					
Query Match	35.6%	Score 536.5;	DB 2;	Length 328;				
Best Local Similarity	43.9%	Pred. No. 1e-32;						
Matches	118	Conservative	44;	Mismatches 104;	Indels 3;	Gaps 2;		
Qy	9 ITLEYEEQGRHRHIPSMLIIMGLGQLIDWPPEBPIRGLAERGFVICPDNRDAGLSTKLEG	68			Db	141	IKYPSVRSLGITSTGSSKRVPETSTRKLFRKALRHFSPG	200
Db	36 VOLAYQSIIGRETDPAVLVIMLGQLIDWPDEVTLGLCRQGRFVRPDNRDGLSAWRQB	95			Qy	189	-LDREKCLALDVRSKLERCL-CPEGTORQALLQSGSRVKLRRIAVPTLVISGAEDPL	245
Qy	9 VPKPNIARVPLIASMGLKPRVPYTLDDMALDTYGLMDALGISTHVGVSMSGMIAQILG	128			Db	201	YNVDBEFSRKLAQEQLRANDYPQGMRLQIAILSRSREECLKTITPLIIGMIDDEV	260
Db	96 VPVSLITYGVLRHRLGLPVSAPIGLRMDAORTLALMARLQVERFHVLGVSMGGMIAQHMA	155			Qy	246	LPYQCCRDIADI-POARFELLEGMDIPIERSHPIRIELIA 286	
Qy	129 AKHGERVKSLSMITSSNPRMPAPRQVLFQEMRVPKSMDEGWIKYNLELLTTGSP-	187			Db	261	VFYQNGLQIAEVGPRLKVIVPMGEHEIPVLMPSISQEA 302	
Db	156 DLAPERVSLTIMITSSAAGLGPSAAL-KLIAQREAGSREVAIRQVEILLAASSPQ	214			Qy	188	-GLDREKCLALDVRSKIERCLCPBTGQTLAQOLAILOSGSRVKLRRIAVPTLVISGAEDPL	246

Search completed: April 13, 2006, 12:59:18
 Job time : 234 secs

Copyright (c) 1993 - 2006 Biocceleteration Ltd.

GenCore version 5.1.7

Run on: April 13, 2006, 12:59:33 ; Search time 47 Seconds
 (without alignments)

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Score: 1509

Exact score: 1 MAQVRKANGTITLEYEEQGHRH.....ERHIPPLIELIAGHAARAAEA 294

Sequence:

protein - protein search, using SW model

Search time: US-10-606-490DD-2

Database: 517,163 Million cell updates/sec

Sequence 1: US-08-232-519-2

Sequence 2: APPL

Sequence 3: APPL

Sequence 4: APPL

Sequence 5: APPL

Sequence 6: APPL

Sequence 7: APPL

Sequence 8: APPL

Sequence 9: APPL

Sequence 10: APPL

Sequence 11: APPL

Sequence 12: APPL

Sequence 13: APPL

Sequence 14: APPL

Sequence 15: APPL

Sequence 16: APPL

Sequence 17: APPL

Sequence 18: APPL

Sequence 19: APPL

Sequence 20: APPL

Sequence 21: APPL

Sequence 22: APPL

Sequence 23: APPL

Sequence 24: APPL

Sequence 25: APPL

Sequence 26: APPL

Sequence 27: APPL

Sequence 28: APPL

Sequence 29: APPL

Sequence 30: APPL

Sequence 31: APPL

Sequence 32: APPL

Sequence 33: APPL

Sequence 34: APPL

Sequence 35: APPL

Sequence 36: APPL

Sequence 37: APPL

Sequence 38: APPL

Sequence 39: APPL

Sequence 40: APPL

Sequence 41: APPL

Sequence 42: APPL

Sequence 43: APPL

Sequence 44: APPL

Sequence 45: APPL

Sequence 46: APPL

Sequence 47: APPL

Sequence 48: APPL

Sequence 49: APPL

Sequence 50: APPL

Sequence 51: APPL

Sequence 52: APPL

Sequence 53: APPL

Sequence 54: APPL

Sequence 55: APPL

Sequence 56: APPL

Sequence 57: APPL

Sequence 58: APPL

Sequence 59: APPL

Sequence 60: APPL

Sequence 61: APPL

Sequence 62: APPL

Sequence 63: APPL

Sequence 64: APPL

Sequence 65: APPL

Sequence 66: APPL

Sequence 67: APPL

Sequence 68: APPL

Sequence 69: APPL

Sequence 70: APPL

Sequence 71: APPL

Sequence 72: APPL

Sequence 73: APPL

Sequence 74: APPL

Sequence 75: APPL

Sequence 76: APPL

Sequence 77: APPL

Sequence 78: APPL

Sequence 79: APPL

Sequence 80: APPL

Sequence 81: APPL

Sequence 82: APPL

Sequence 83: APPL

Sequence 84: APPL

Sequence 85: APPL

Sequence 86: APPL

Sequence 87: APPL

Sequence 88: APPL

Sequence 89: APPL

Sequence 90: APPL

Sequence 91: APPL

Sequence 92: APPL

Sequence 93: APPL

Sequence 94: APPL

Sequence 95: APPL

Sequence 96: APPL

Sequence 97: APPL

Sequence 98: APPL

Sequence 99: APPL

Sequence 100: APPL

Sequence 101: APPL

Sequence 102: APPL

Sequence 103: APPL

Sequence 104: APPL

Sequence 105: APPL

Sequence 106: APPL

Sequence 107: APPL

Sequence 108: APPL

Sequence 109: APPL

Sequence 110: APPL

Sequence 111: APPL

Sequence 112: APPL

Sequence 113: APPL

Sequence 114: APPL

Sequence 115: APPL

Sequence 116: APPL

Sequence 117: APPL

Sequence 118: APPL

Sequence 119: APPL

Sequence 120: APPL

Sequence 121: APPL

Sequence 122: APPL

Sequence 123: APPL

Sequence 124: APPL

Sequence 125: APPL

Sequence 126: APPL

Sequence 127: APPL

Sequence 128: APPL

Sequence 129: APPL

Sequence 130: APPL

Sequence 131: APPL

Sequence 132: APPL

Sequence 133: APPL

Sequence 134: APPL

Sequence 135: APPL

Sequence 136: APPL

Sequence 137: APPL

Sequence 138: APPL

Sequence 139: APPL

Sequence 140: APPL

Sequence 141: APPL

Sequence 142: APPL

Sequence 143: APPL

Sequence 144: APPL

Sequence 145: APPL

Sequence 146: APPL

Sequence 147: APPL

Sequence 148: APPL

Sequence 149: APPL

Sequence 150: APPL

Sequence 151: APPL

Sequence 152: APPL

Sequence 153: APPL

Sequence 154: APPL

Sequence 155: APPL

Sequence 156: APPL

Sequence 157: APPL

Sequence 158: APPL

Sequence 159: APPL

Sequence 160: APPL

Sequence 161: APPL

Sequence 162: APPL

Sequence 163: APPL

Sequence 164: APPL

Sequence 165: APPL

Sequence 166: APPL

Sequence 167: APPL

Sequence 168: APPL

Sequence 169: APPL

Sequence 170: APPL

Sequence 171: APPL

Sequence 172: APPL

Sequence 173: APPL

Sequence 174: APPL

Sequence 175: APPL

Sequence 176: APPL

Sequence 177: APPL

Sequence 178: APPL

Sequence 179: APPL

Sequence 180: APPL

Sequence 181: APPL

Sequence 182: APPL

Sequence 183: APPL

Sequence 184: APPL

Sequence 185: APPL

Sequence 186: APPL

Sequence 187: APPL

Sequence 188: APPL

Sequence 189: APPL

Sequence 190: APPL

Sequence 191: APPL

Sequence 192: APPL

Sequence 193: APPL

Sequence 194: APPL

Sequence 195: APPL

Sequence 196: APPL

Sequence 197: APPL

Sequence 198: APPL

Sequence 199: APPL

Sequence 200: APPL

Sequence 201: APPL

Sequence 202: APPL

Sequence 203: APPL

Sequence 204: APPL

Sequence 205: APPL

Sequence 206: APPL

Sequence 207: APPL

Sequence 208: APPL

Sequence 209: APPL

Sequence 210: APPL

Sequence 211: APPL

Sequence 212: APPL

Sequence 213: APPL

Sequence 214: APPL

Sequence 215: APPL

Sequence 216: APPL

Sequence 217: APPL

Sequence 218: APPL

Sequence 219: APPL

Sequence 220: APPL

Sequence 221: APPL

Sequence 222: APPL

Sequence 223: APPL

Sequence 224: APPL

Sequence 225: APPL

Sequence 226: APPL

Sequence 227: APPL

Sequence 228: APPL

Sequence 229: APPL

Sequence 230: APPL

Sequence 231: APPL

Sequence 232: APPL

Sequence 233: APPL

Sequence 234: APPL

Sequence 235: APPL

Sequence 236: APPL

Sequence 237: APPL

Sequence 238: APPL

Sequence 239: APPL

Sequence 240: APPL

Sequence 241: APPL

Sequence 242: APPL

Sequence 243: APPL

Sequence 244: APPL

Sequence 245: APPL

Sequence 246: APPL

Sequence 247: APPL

Sequence 248: APPL

Sequence 249: APPL

Sequence 250: APPL

Sequence 251: APPL

Sequence 252: APPL

Sequence 253: APPL

Sequence 254: APPL

Sequence 255: APPL

Sequence 256: APPL

Sequence 257: APPL

Sequence 258: APPL

Sequence 259: APPL

Sequence 260: APPL

Sequence 261: APPL

Sequence 262: APPL

Sequence 263: APPL

Sequence 264: APPL

Sequence 265: APPL

Sequence 266: APPL

Sequence 267: APPL

Sequence 268: APPL

Sequence 269: APPL

Sequence 270: APPL

Sequence 271: APPL

Sequence 272: APPL

Sequence 273: APPL

Sequence 274: APPL

Sequence 275: APPL

Sequence 276: APPL

Sequence 277: APPL

Sequence 278: APPL

Sequence 279: APPL

Sequence 280: APPL

Sequence 281: APPL

Sequence 282: APPL

Sequence 283: APPL

Sequence 284: APPL

Sequence 285: APPL

Sequence 286: APPL

Sequence 287: APPL

Sequence 288: APPL

Sequence 289: APPL

Sequence 290: APPL

Sequence 291: APPL

Sequence 292: APPL

Sequence 293: APPL

Sequence 294: APPL

Sequence 295: APPL

Sequence 296: APPL

Sequence 297: APPL

Sequence 298: APPL

Sequence 299: APPL

Sequence 300: APPL

```

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : Issued Patents AA:*
  1: /cgn2_6_ptodata/1/iaa/5_COMB.pep:*
  2: /cgn2_6_ptodata/1/iaa/6_COMB.pep:*
  3: /cgn2_6_ptodata/1/iaa/7_COMB.pep:*
  4: /cgn2_6_ptodata/1/iaa/8_COMB.pep:*
  5: /cgn2_6_ptodata/1/iaa/9_COMB.pep:*
  6: /cgn2_6_ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

; Sequence 5739, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACTINOMYCESES
; FILE REFERENCE: GPC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5739
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US/09-328-352-5739

```

Result	No.	Score	Query Match Length	DB ID	Description
Best Local Similarity 46.9% ; Matches 134; Conservative 49; Mismatches 98; Pre. no. 3.e-5/	1	607.5	40.3	322 US-09-3228-352-5739	Sequence 5739, Ap
	2	562.5	37.3	422 US-09-252-591A-21999	Sequence 21999, A
	3	483	32.0	360 US-09-540-336-3609	Sequence 3609, Ap
	4	314.5	20.8	267 US-08-935-663-10	Sequence 10, Appl
	5	314.5	20.8	267 US-09-594-865-10	Sequence 10, Appl
	6	314.5	20.8	267 US-10-33-078-10	Sequence 10, Appl
	7	314.5	20.8	267 US-10-763-333-10	Sequence 10, Appl
	8	262.5	17.4	247 US-09-902-840-14883	Sequence 14883, A
	9	192	12.7	287 US-09-252-591A-22466	Sequence 22466, A
	10	189.5	12.6	251 US-09-345-169-4	Sequence 4, Appl
	11	189	12.5	268 US-09-252-591A-32242	Sequence 32242, A
	12	185	12.3	265 US-09-902-540-11639	Sequence 11639, A
	13	183	12.1	289 US-09-469-11A-6	Sequence 6, Appl
	14	183	12.1	289 US-09-446-681-6	Sequence 6, Appl
	15	182.5	12.1	271 US-09-902-540-12298	Sequence 12298, A
	16	181.5	12.0	264 US-09-134-301C-5592	Sequence 5592, Ap
	17	180	11.9	338 US-09-252-591A-32574	Sequence 32574, A
	18	175	11.6	261 US-09-902-540-13754	Sequence 13754, A
	19	174	11.5	334 US-09-902-540-11426	Sequence 11426, A
	20	174	11.5	786 US-09-252-591A-32352	Sequence 32352, A
	21	173.5	11.5	271 US-09-328-352-7546	Sequence 7546, Ap
	22	168	11.1	281 US-09-902-540-11020	Sequence 11020, A
	23	163	10.8	287 US-09-902-540-15478	Sequence 15478, A
	24	162.5	10.8	275 US-09-902-540-15896	Sequence 15896, A
	25	157	10.4	320 US-10-272-190-6	Sequence 6, Appl
	26	156.5	10.4	274 US-09-252-591A-21590	Sequence 21590, A
	27	155.5	10.2	276 US-09-355-166-9	Sequence 9, Appl
RESULT 2					
					US-09-252-991A-21999
					; Sequence 21999, Application US/09252991A
					; Patent No. 65587195
					; GENERAL INFORMATION:
					; APPLICANT: Marc J. Rubenfield et al.
					; TITLER OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUD

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252,931A
 CURRENT FILING DATE: 1999-02-18
 PRIORITY NUMBER: US 60/074,788
 PRIOR APPLICATION NUMBER: US 60/02-18
 PRIOR FILING DATE: 1998-02-18
 PRIORITY NUMBER: US 60/094,190
 PRIORITY FILING DATE: 1998-07-27
 SEQ ID NO: 33142
 LENGTH: 422
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-21999

Query Match Score 37.3%; DB 2; Length 422;

Best Local Similarity 43.1%; Pred. No. 3.5e-52;
 Matches 125; Conservative 45; Mismatches 117; Indels 3; Gaps 2;

4 VKANGITLVEEQGRHPSMLIGGLQDIDWPEEFIRGLAERGPFRVICFDNRDAGLS 63

125 VELGDVRLAQSIGRDSDPALLWGLGQLIHPDEVSCEQGFRTRIDNRDGLS 184

64 TKLEGVKPNIARYFLLASMGLKPRVPTLDDMDALDTYGLMDALGIESTHYGVSMGMI 123

185 AWNPVPSSRLTYEVRYGLPVAPSAPTLTDAGDLHLDIPOAHVLGASMGM 244

124 AQILAKHGERVKSLTIMTSSGNPRMPAPRQVLFQKMRVPKSMDEKEEWIKYNLELT 183

245 AQHADMAQPLLSLTWNVSGAEGLPAPSESLULLAR-REASAQAVEQADLIA 303

184 IGSPRL--DREKLALDVRAKSIERCLCPECTOROLAILLGSGRSVLLRRAEVTLVIGA 241

304 LGSPVDRDQRQLLQAAASYDRAFNPGYQRQLLAILEPSRVPLNLQVPTLVIGT 363

242 EDPLLPYQCGRDIAHDHIGPARFELIEGMHDPERHPIELIJAGHAA 291

364 ADPLLPVMEGVHVAHRSSELKJPGLHRFQEAFKEPLLAAVVPUKA 413

RESULT 3
 US-09-540-236-3609
 Sequence 3609, Application US/09540236
 Patent No. 6673310
 GENERAL INFORMATION:
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
 FILE REFERENCE: 2709, 2005-001
 CURRENT APPLICATION NUMBER: US/09/540,236
 SEQ ID NO: 3609
 LENGTH: 360
 TYPE: PRT
 ORGANISM: *M.catarrhalis*
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION (250)
 OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
 US-09-540-236-3609

Query Match

Score 37.3%; DB 2; Length 360;

Best Local Similarity 37.3%; Pred. No. 1.1e-43;
 Matches 107; Conservative 61; Mismatches 113; Indels 6; Gaps 3;

8 GITLBYEEQGRHPSMLIGGLQDIDWPEEFIRGLAERGPFRVICFDNRDAGLSK- 65

42 GIKLCKVEAGCNPPMITEITGQGNSWFSQDPLKRPFDVFRDNRDGLSKIQ 101

66 LEGYKPKPNIARYFLLASMGLKPR---VPVTDMDALDTYGLMDALGLESTHVGVSNGM 122

102 IDGLPLRNLTFKQMLKMQAQLSNRSEPVAYLTDMAEDARLKTMOHLNVNLIGASNGM 161

Qy 123 IAOILGAKHGERVKSLTIMTSSGNPRMPAPRQVLFQKMRVPKSMDEKEEWIKYNLELT 182
 Db 162 IAQIVAAQYPKTKIKNVILFSTSNRAFLRPNPKQFMTFVRRBHSERDMYHSVVWNT 221
 Qy 183 TIGSPG-LDREKLALDVRAKSIERCLCPECTOROLAILLGSGRSVLLRRAEVTLVIGA 241
 Db 222 AVGSPGHIDIKGTRIAEKYORNFPLXVSQOITALASRSRLFTQIRANTLVIGN 281
 Qy 242 EDPLLPYQCGRDIAHDHIGPARFELIEGMHDPERHPIELIJAGH 288
 Db 282 KDSIVAPNHGKTLAKVTSNAREVFLDGMGHDLPNYYPYLNGLISEH 328

RESULT 4
 US-09-335-263-10

Query Match Sequence 10, Application US/08935263A
 Best Local Similarity 43.1%; Pred. No. 6117669
 Matches 92; Conservative 43; Mismatches 14; Indels 39; Gaps 9;

GENERAL INFORMATION:

APPLICANT: Furuchi, Yasuhiro

APPLICANT: Hoshino, Tatsuo

APPLICANT: Kimura, Hitoshi

APPLICANT: Kiyasu, Tatsuya

APPLICANT: Nagashashi, Yoshiie

TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES

CURRENT APPLICATION NUMBER: US/08/935,263A

CURRENT FILING DATE: 1997-09-22

EARLIER APPLICATION NUMBER: EP 96115540.5

NUMBER OF SEQ ID NOS: 23

SEQUENCE ID NO: 10

LENGTH: 267

TYPE: PRT

ORGANISM: Kurthia sp.

US-09-335-263-10

Query Match Score 20.8%; DB 2; Score 314.5%; DB 2;
 Best Local Similarity 33.1%; Pred. No. 1.3e-25;
 Matches 92; Conservative 43; Mismatches 14; Indels 39; Gaps 9;

Qy 1 MAQVKANGITLVEEQGRHPSMLIIMGQLIDWPEEFIRGLAERGPFRVICFDNRDAGLS 60

Db 1 MPFVNHDNESELYEV--HGQGDPBLIUNGQGYNLSNW-HRTVFLAKR-FKVTVFDRGV 56
 57 GSNS-----REQPQSIEMMAEDARAVLDAVSVDSAHVGYSMG 95

61 GLSTKLEGVKPNIARYFLLASMGLKPRVPTLDDMDALDTYGLMDALGIESTHVGVSNGM 120

Db 121 GMIAQILGAKHGERVKSLTIMTSSGNPRMPAPRQV--LOKFMRVYPSMKEEW---- 173
 96 GMIAQRQLITYPERSVLSVLGETTAGTTTQSPSETSTMVSASLTGSPDNWLAAP 155

174 IKYNLELITTCGPGDREKLALDVRAKSIERCLCPECTOROLAILLGSGRSVLLRRAEVTLVIGA 233

Db 156 IVYSQATEK-HPELIQE---DQKRRIITPPSAYLSQIQCATHDTSNS-LDKINI 208

234 PTUVISGAEDPLLPYQCGRDIAHDHIGPARFELIEGMCH 271
 Qy 235 IATLGAQKAKHGERVKSLTIMTSSGNPRMPAPRQV--LOKFMRVYPSMKEEW---- 173
 Db 209 PTIINHGADNLVPPYENGKMLAERIQQSQHTVSCAGH 246

RESULT 5
 US-09-554-185-10

Query Match Sequence 10, Application US/09594185
 Best Local Similarity 37.3%; Pred. No. 6365388
 Matches 107; Conservative 61; Mismatches 113; Indels 6; Gaps 3;

GENERAL INFORMATION:

APPLICANT: Furuchi, Yasuhiro

APPLICANT: Hoshino, Tatsuo

APPLICANT: Kimura, Hitoshi

APPLICANT: Kiyasu, Tatsuya

APPLICANT: Nagashashi, Yoshiie

TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
FILE REFERENCE: Biotin Genes
CURRENT APPLICATION NUMBER: US/09/594,185
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 08/935,263
PRIOR FILING DATE: 1997-09-22
PRIOR APPLICATION NUMBER: EP 96115540.5
PRIOR FILING DATE: 1996-09-27
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 10
LENGTH: 267
TYPE: PRT
ORGANISM: Kurthia sp.
US -09-594-185-10

Query Match 20.8%; Score 314.5; DB 2; Length 267;
Best Local Similarity 33.1%; Pred. No. 1.3e-25;
Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;

RESULT 6
US-09-594-185-10
; Sequence 10, Application US/10033078
; Patent No. 672354
; GENERAL INFORMATION:
; APPLICANT: Furuchi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuya
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; CURRENT APPLICATION NUMBER: US/10/033,078
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 09/594,185
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: EP 96115540.5
; PRIOR FILING DATE: 1996-09-27
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Kurthia sp.

Query Match 20.8%; Score 314.5; DB 2; Length 267;
Best Local Similarity 33.1%; Pred. No. 1.3e-25;
Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;

RESULT 7
US-10-763-933-10
; Sequence 10, Application US/10763933
; Patent No. 6955906
; GENERAL INFORMATION:
; APPLICANT: Furuchi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuya
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; CURRENT APPLICATION NUMBER: US/10/763,933
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/033,078
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 09/594,185
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: EP 96115540.5
; PRIOR FILING DATE: 1996-09-27
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 10
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Kurthia sp.

Query Match 20.8%; Score 314.5; DB 2; Length 267;
Best Local Similarity 33.1%; Pred. No. 1.3e-25;
Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;

RESULT 8
1 MAQVKANGTILEYBQGRHRRPHPSMLIMGLGQLIDWPBEFIRLAERFRVICPDNRDA 60
Db 1 MPFVNHDNESLYYEV-HGQGDPLIIMGJGYNSSW-HRTVPTLAKR-FKVIVFDNRGV 56
Db 61 GLSTKLEGVKPNTARVELLASMGLKPRPYTLDDMALDTVGMLDALGIESTHVGVSMG 120
Db 96 GMAQRLAITYPERVSLVLGCTTAGGTHIQPSPEISTLMVRASLTCSPRDNAWLAAP 155
Db 57 GKSS-----KPEQPSIEMMAEARDARAVLDASVDSARYGISMG 95
Db 121 GMAQILGAHKGERVKSUTLIMTSSGNPRMPAPRQV--LQKMRVPKSMDKEW----
Db 96 GMAQRLAITYPERVSLVLGCTTAGGTHIQPSPEISTLMVRASLTCSPRDNAWLAAP 155
Db 174 IKNLELLITIGSPGLDREKLALDVRKSIERCLCPGTORQALNLSQGSRVKLRRIAV 233
Db 156 IVYSAFIEK--HPELIQS---DIOKRIEITTPSAYSLSQACLTHTSNE-LDKINI 208
Qy 234 PTLYISGAEDPLLPYQCRDIADHIPGARFELIGMGH 271
Db 209 PTLYHGDAADNLVPYENGKMLAERIQSQFHTVSCAGH 246

Query Match 20.8%; Score 314.5; DB 2; Length 267;
Best Local Similarity 33.1%; Pred. No. 1.3e-25;
Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;

RESULT 9
1 MAQVKANGTILEYBQGRHRRPHPSMLIMGLGQLIDWPBEFIRLAERFRVICPDNRDA 60
Db 1 MPFVNHDNESLYYEV-HGQGDPLIIMGJGYNSSW-HRTVPTLAKR-FKVIVFDNRGV 56
Db 61 GLSTKLEGVKPNTARVELLASMGLKPRPYTLDDMALDTVGMLDALGIESTHVGVSMG 120
Db 96 GMAQRLAITYPERVSLVLGCTTAGGTHIQPSPEISTLMVRASLTCSPRDNAWLAAP 155
Db 57 GKSS-----KPEQPSIEMMAEARDARAVLDASVDSARYGISMG 95
Db 121 GMAQILGAHKGERVKSUTLIMTSSGNPRMPAPRQV--LQKMRVPKSMDKEW----
Db 96 GMAQRLAITYPERVSLVLGCTTAGGTHIQPSPEISTLMVRASLTCSPRDNAWLAAP 155
Db 174 IKNLELLITIGSPGLDREKLALDVRKSIERCLCPGTORQALNLSQGSRVKLRRIAV 233
Db 156 IVYSAFIEK--HPELIQS---DIOKRIEITTPSAYSLSQACLTHTSNE-LDKINI 208
Qy 234 PTLYISGAEDPLLPYQCRDIADHIPGARFELIGMGH 271
Db 209 PTLYHGDAADNLVPYENGKMLAERIQSQFHTVSCAGH 246

US-09-902-540-14883
i Sequence 14883, Application US/0902540
i Patent No. 6833447
i GENERAL INFORMATION:
i APPLICANT: Goldman, Barry S.
i APPLICANT: Hinkle, Gregory J.
i APPLICANT: Slater, Steven C.
i APPLICANT: Wiesand, Roger C.
i TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
i FILE REFERENCE: 38-10(15849)B
i CURRENT APPLICATION NUMBER: US/09/902,540
i CURRENT FILING DATE: 2001-07-10
i PRIOR APPLICATION NUMBER: 60/217,883
i PRIOR FILING DATE: 1998-07-10
i NUMBER OF SEQ ID NOS: 16825
i SEQ ID NO 14883
i LENGTH: 247
i TYPE: PRT
i ORGANISM: Myxococcus xanthus
i US-09-902-540-14883

Query Match 17.4%; Score 262.5; DB 2; Length 247;
 Best Local Similarity 30.3%; Pred. No. 5.1e-20;
 Matches 79; Conservative 38; Mismatches 107; Indels . 37; Gaps 7;

Db 45 LAERGFRVTCFVNDAGLSTKLEGVKPKNIAVRFLASGLKPRVPYTLDDMALTIVGL 104
Qy ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 4 LARAGRFRVTCFVNDAGLSTKLEGVKPKNIAVRFLASGLKPRVPYTLDDMALTIVGL 104
Qy 105 DALGIESTHVGVSMMGMAQILGAKHGHGRVKSLTLM--ITSSGNPRMPAPRPPQVLOK 161
Db 46 DGYGTERAHLVGMGLQQLVALKYPPRVLSTLISQIPEPDPGMDDPAVLAAH 105
Qy 162 MRVP--KSMDKEENIKYNEL-LTTIGSP--GLDREKLADYRKSIERCLCPGTOROLA 216
Db 106 QRAATLAWNSBEEAIGFQEVLSRUCVGRARRSFDEARYARAQDYRLEALAPO---C 159
Qy 217 ALQSGSRVKL---LRRIAVPFLVISGAEDPPLPYQCRDIAHDIGARFELIEGMGH 271
Db 160 ALNHEAGLSSCQEWTGRTRETEAUPLVIHQSSVDPVTDHARGVALSRAVKGACLYTLHDAGH 219
Qy 272 DIPERHIIPLIELLAGHAAA 292
Db 220 DLHFDDEWETMTRAITAHTSRA 240

Query Match 12.6%; Score 189.5; DB 2; Length 251;
 Best Local Similarity 29.1%; Pred. No. 4.3e-12;
 Matches 76; Conservative 35; Mismatches 99; Indels 51; Gaps 9;

Db 50 FRVICFONRDAGLSTKLEGVKPKNIAVRFLASGLKPRVPYTLDDMALTIVGLDALIG 109
Qy ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 FRYTIALDRLGFGESSRPSDL-----ADYRFDDAEDLEALLDALGL 41

Db 110 ESTHV--VGVSMMGMAQILGAKHGHGRVKSLTLM--ITSSGNPRMPAPRPPQVLOKFMRYPK- 166
Qy :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 42 DRPVLYGHSMGALAYAARYPERVKALVYST-----PAPGLSSRLPRLGPNL 94

Db 167 -----SMDREWKYNNLELLTIGSPGL-DREKLADYRKSIERCLCPGTQR 213
Qy ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 95 EGIILLANFENLRSVEALLGRALKOFFLGRPFVSDFLKQABDWSSLARPGETDGSDG 154

Db 214 QLAALIOSGSRVK---LLRRIAVPFLVISGAEDPPLPYQCRDIAHDIGARFELIEGM 269
Qy ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 155 LIGYAVALGKLIQWDRSALKDOKVPTLVWGDPLPLVKASEKLSALFPNAEVVVIDA 214

Db 270 GH---DIPERHIIPLIELLAGHAAA 286
Qy ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 215 GHLLALEKPE-EVAELIKFLA 234

Query Match 12.7%; Score 192; DB 2; Length 287;
 Best Local Similarity 26.9%; Pred. No. 2.8e-12;
 Matches 71; Conservative 38; Mismatches 111; Indels 44; Gaps 6;

US-09-252-991A-22466
i Sequence 22466, Application US/09252991A
i Patent No. 6551195
i GENERAL INFORMATION:
i APPLICANT: Marc J. Rubenfield et al.
i TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
i FILE REFERENCE: 10/196,136
i CURRENT APPLICATION NUMBER: US/09/252,991A
i CURRENT FILING DATE: 1999-02-18
i PRIOR APPLICATION NUMBER: US 60/074,788
i PRIOR FILING DATE: 1998-02-18
i PRIOR APPLICATION NUMBER: US 60/094,190
i PRIOR FILING DATE: 1998-07-27
i NUMBER OF SEQ ID NOS: 33142
i SEQ ID NO 22466
i LENGTH: 287
i TYPE: PRT
i ORGANISM: Pseudomonas aeruginosa
i US-09-252-991A-22466

Query Match 12.7%; Score 192; DB 2; Length 287;
 Best Local Similarity 26.9%; Pred. No. 2.8e-12;
 Matches 71; Conservative 38; Mismatches 111; Indels 44; Gaps 6;

RESULT 11
 US-09-252-991A-32242
i Sequence 32242, Application US/09252991A
i Patent No. 6551195

6 ANGITLEYEBQGRHRHPSMSILIMLGQQLIDWPREFIRGLAERGFRYCFDNRDAGLSTK 65
i Qy

GENERAL INFORMATION:
 i APPLICANT: Rubenfield et al.
 i TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 i FILE REFERENCE: 107196 135
 i CURRENT APPLICATION NUMBER: US/09/252, 921A
 i CURRENT FILING DATE: 1999-02-18
 i PRIOR APPLICATION NUMBER: US 60/074, 788
 i PRIOR FILING DATE: 1998-02-18
 i PRIOR APPLICATION NUMBER: US 60/094, 190
 i PRIOR FILING DATE: 1998-07-27
 i NUMBER OF SEQ ID NOS: 33142
 i SEQ ID NO: 32242
 i LENGTH: 268
 i TYPE: PRT
 i ORGANISM: Pseudomonas aeruginosa
 i US-09-252-991A-32242

Query Match 12.5%; Score 189; DB 2; Length 268;
 Best Local Similarity 25.5%; Pred. No. 5.3e-12; Gaps 10;
 Matches 75; Conservative 38; Mismatches 115; Indels 66; Gaps 10;

Qy 11 LEYEQGRHRPHPSMILLIMGLGGQLIDWPEERIRGLAERGFRVICPDNRDAGLSTKLEGYK 70
 Db 16 LNSLSEPGAPAVPLLSNLSLGTDLGMWDQT-IPALTAH-FRVLRYDTDRGHGSLVTPG-- 71

Qy 71 KPNIARVFLLASMGKLPKRVPYTLDDMALDTGLMDALGISTTHVGSNSCGMIAQILGAK 130
 Db 72 -----PVAIGOLGADVALLDALELPRVHFCGLSMCGGLIGOWLGH 112

Qy 131 HGERVTKSLLIMITSS-----GNPRMPAPRQVL---QKEMRVPKSMDKEWIKYNEL 180
 Db 113 AGERLGRVLVLCNTAAKIASDEWNTIDT---VKGGEQAMRVRDAYSARWF---- 162

Qy 181 LTIGSPGLDREKLAUDVRSKSIERCLCPECTORQLAAILQSRSVYKLRRIAVPTLVISG 240
 Db 163 --TAGF--AERPAQVERIVMLAATSPQYAANCAAVRDADFR-EQLGIVQAPTIVAG 217

Qy 241 ABPLPLPYQCRDIADHIGARFELIGMHDIPERHPIPLIELAGHAAAEEA 294
 Db 218 SHDAVTTPDNARFMQARIADA-----OLVEFAAAHLSNEA 253

RESULT 12
 US-09-902-540-11639
 i Sequence 11639, Application US/09902540
 i GENERAL INFORMATION:
 i APPLICANT: Goldman, Barry S.
 i APPLICANT: Hinkle, Gregory J.
 i APPLICANT: Slater, Steven C.
 i APPLICANT: Wiegand, Roger C.
 i TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 i FILE REFERENCE: 38-10/158491B
 i CURRENT APPLICATION NUMBER: US/09/902, 540
 i CURRENT FILING DATE: 2001-07-10
 i PRIOR APPLICATION NUMBER: 60/217, 883
 i SEQ ID NO: 11639
 i LENGTH: 265
 i TYPE: PRT
 i ORGANISM: Myxococcus xanthus
 i US-09-902-540-11639

Query Match 12.3%; Score 185; DB 2; Length 265;
 Best Local Similarity 26.7%; Pred. No. 1.4e-11;
 Matches 77; Conservative 38; Mismatches 121; Indels 52; Gaps 9;

Qy 1 MAQVXKANGITLLEYEBCGRHRPHPSMILLI-MGIGGQDIDWPEEFTRGLAERGFRVICFDFR 58
 Db 1 MLTVTVGDVPLHYRDG-KSPPVLLHAPPLNGSTFD--KQVRLSGR-YRFIIPDR 54

RESULT 13
 US-09-46-211A-6
 i Sequence 6, Application US/09469211A
 i Patent No. 666054
 i GENERAL INFORMATION:
 i APPLICANT: J. Turk
 i ARCHER, J.
 i TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN EUKARYOTES
 i FILE REFERENCE: 9341-021
 i CURRENT APPLICATION NUMBER: US/09/469, 211A
 i CURRENT FILING DATE: 1999-12-22
 i PRIORITY APPLICATION NUMBER: UK 9828660-2
 i PRIORITY FILING DATE: 1998-12-24
 i NUMBER OF SEQ ID NOS: 19
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO 6
 i LENGTH: 289
 i TYPE: PRT
 i ORGANISM: Rhodococcus sp.
 i US-09-46-211A-6

Query Match 12.1%; Score 183; DB 2; Length 289;
 Best Local Similarity 24.3%; Pred. No. 2.7e-11;
 Matches 68; Conservative 43; Mismatches 123; Indels 46; Gaps 9;

Qy 4 VKANGITLLEYEBCGRHRPHPSMILLIMGLGQOLIDWPEBFIRGLAEGG--FRVICFPNRDAG 61
 Db 22 IQAGPYRTRYLHAGDSKSPKTLLHGHGTH---AEAYTRNLRSHEHNWTAIFIGH 77

Qy 62 LSTKLEGVKPNIARVFLLASMGKLPKRVPYTLDDMALDTGLMDALGISTTHVGSNSCGMGG 121
 Db 78 YST-----KPDHPLEIKHYIDHVQLLDIGVEKAFSOBSSLGG 116

Qy 122 MIAQILGAKHGERVKSLLIMITSSGGNPRMPAPRQVLQKEMRVPKSMDKE--EWIKYNL 178
 Db 117 WTVQAFADHDPKEDYDRIVLN-TNGGT---MANPOVMERLYTNEAKADPSWENVKARL 171

Qy 179 ELL--TTIGSPGLDREKLAUDVRSKSIERCLCPECTORQLAAILQSRSVYKLRRIAVPTLVISG 231
 Db 172 EWLMADPTWTDLIRTOAIFOQPDWLKACENMMALQDETRKNMTDAT---LNGI 227

Qy 232 AVPLVIVISGAEDPLPYQCRDIADHIGARFELIGMHDIPERHPIPLIELAGHAAAEEA 271
 Db 228 TVPANVLTWTTKOPSGPVDEAKRASHIPGAKLAIMENCGH 267

RESULT 14
 US-09-44-681-6
 i Sequence 6, Application US/09446681
 i Patent No. 6849442
 i GENERAL INFORMATION:
 i APPLICANT: Archer, John AC
 i APPLICANT: Summers, David K
 i APPLICANT: Roland, Herve J
 i APPLICANT: Powell, Justin AC
 i TITLE OF INVENTION: Biosensor materials and methods

FILE REFERENCE: 0380-P02083-US0
 CURRENT APPLICATION NUMBER: US 09/446,681
 CURRENT FILING DATE: 2000-03-14
 PRIOR APPLICATION NUMBER: PCT/GB98/01893
 PRIOR FILING DATE: 1998-06-29
 PRIOR APPLICATION NUMBER: GB 9713666 .7
 PRIOR FILING DATE: 1997-06-27
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 289
 TYPE: PRT
 ORGANISM: Rhodococcus corallina
 US -09-446-681-6

Query Match 12.1%; Score 183; DB 2; Length 289;
 Best Local Similarity 24.3%; Pred. No. 2.7e-11;
 Matches 68; Conservative 43; Mismatches 123; Indels 46; Gaps 9;

Qy 4 VRANGITLBYEQGHRHPPSNLLINGLGQDIDWDBEFGLAGRG--PRVICPDNRDAG 61
 Db 22 IAGPYRTYHLAGSSKPTILLHGITHG--AEAYRNLRHSEHNWALDFIGH 77

Qy 62 LSTKLEGVKKPNIARVFLASMGKPRVPTLDDMADTGLMDALGIBESTHYVGVSNGG 121
 Db 78 YST-----KPDHPDEIKHYIDHVLQQLDAIGYKASFSGESLIG 116

Qy 122 MIAQILGARGERVLSLTMITSSGNPRMPAPRPOVLFQMRVPKSMDKE--EWIKNL 178
 Db 117 WVTAQFAHDPEKVDRIVN-TMGET---MANPQYMERLYTSMEAARDPSWERVKRL 171

Qy 179 ELL---TITISPGLOREKLAL---DVRKSIERCUCPEGTORQLAAILGSRSVKKRL 231
 Db 172 EWLADPTWTDLIRTRQIFQQPDWLKACMMALOLETRRNMTDAT---LNGI 227

Qy 232 AVPTLVISGAEDPLLPYOCGRDIADHIPGARFELIEGMGH 271
 Db 228 TVPANVLTWTTKDPSPGVDEAKRIASHIPGAKLAINENCGH 267

RESULT 15
 US-09-902-540-12298
 Sequence 12298, Application US/09902540
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US 09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO: 12298
 ; LENGTH: 271
 ; TYPE: PRT
 ; ORGANISM: Myxococcus xanthus
 US -09-902-540-12298

Query Match 12.1%; Score 182.5; DB 2; Length 271;
 Best Local Similarity 26.8%; Pred. No. 2.7e-11; Mismatches 118; Indels 67; Gaps 14;

Qy 1 MAQVKANGTLEYBQGRRHHPSMLIMCHGGOLDWPEEFIRGLAERGSERVICEFDNRDA 60
 Db 1 MPJLQLEESLYFESG--EGTPVLFHQGSSGRDW-EVAPEPLTGR-HRVTPDARGH 56

Qy 61 GLSTKLEGVKKPNIARVFLASMGKPRVPTLDDMADTGLMDALGIBESTHVGVSMG 120
 Db 57 GRSGKPPGA-----YGVPRFARDIAGLCDALGTCGAVGMSMG 95

Search completed: April 13, 2006, 13:00:56
 Job time : 48 secs

Qy 121 GMIAQILGAKHGERVSLTLMITSSGNPRMPAPRPOVLFQMRVPKSMDKEEWIKNL 180
 Db 96 GMGFQLAVIDPELIRS-LVING-----PELVARTLR----RKPERGLRLTL 139

Qy 181 LTTIGS-----PGLDREKL---ALDVRKSTERCLCPEGTOROLAATLQSNSRV 225
 Db 140 LKLIGPSVLAKVLTAPKLFPKPEOALRORALETFSAN-----PDYLRAKGIV-GWSVM 194

Qy 226 KLLRRIAVPTLVISGAEDPLLPYOCGRDIADHIPGARFELIEGMG---HDI PERHIPL 281
 Db 195 RHLLGGITCPVVLASRD-YTPVSTKQAYDILPNAVLQVLSGHSASPHDQDKVADAV 253

Qy 282 IELIAG-HAAAAEA 294
 Db 254 EAFLAGVEDAAADA 267

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 13:10:48 ; Search time 161 Seconds (without alignment(s))

Title: US-10-686-490D-2

Pefect score: 1509

Sequence: 1 MAQVKANGITLLEYEQGHRH.....ERHPRLIELIAGHAAAAEA 294

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Published Applications AA_Main.*

1: /cgn2_6/ptodata/1/pubpaa/us07_PUBCOMB_pep:*

2: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB_pep:*

3: /cgn2_6/ptodata/1/pubpaa/us09_PUBCOMB_pep:*

4: /cgn2_6/ptodata/1/pubpaa/us10_PUBCOMB_pep:*

5: /cgn2_6/ptodata/1/pubpaa/us10_PUBCOMB_pep:*

6: /cgn2_6/ptodata/1/pubpaa/us11_PUBCOMB_pep:*

RESULT 1
US-10-686-490D-2

; Sequence 2, Application US/10686490D
; Publication No. US2005015340441
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Anti-Kaztauskas-Lipases
; FILE REFERENCE: Lea 35 991
; CURRENT APPLICATION NUMBER: US/10/686,490D
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: bacterial

Query Match 100.0%; Score 1509; DB 5; Length 294;
Best Local Similarity 100.0%; Pred. No. 3.6e-145; Indels 0; Gaps 0;

Matches 294; Conservative 0; Mismatches 0;

US-10-686-490D-2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1509	100.0	294	5 US-10-686-490D-2	Sequence 2, Appli
2	314.5	20.8	267	4 US-10-033-078-10	Sequence 10, Appli
3	314.5	20.8	267	4 US-10-763-933-10	Sequence 10, Appli
4	268.5	17.8	273	5 US-10-211-028-165	Sequence 165, Appli
5	227.5	15.1	271	4 US-10-329-079-51	Sequence 51, Appli
6	220.5	14.6	276	4 US-10-282-122A-19054	Sequence 490/54, Appli
7	216.5	14.3	264	4 US-10-329-079-18	Sequence 18, Appli
8	204	13.5	271	3 US-09-976-059-10	Sequence 10, Appli
9	204	13.5	303	4 US-10-156-761-0055	Sequence 80/5, Appli
10	198	13.1	232	3 US-09-896-578-4	Sequence 4, Appli
11	198	13.1	232	3 US-09-971-490-14	Sequence 14, Appli
12	198	13.1	232	4 US-10-289-148-4	Sequence 4, Appli
13	198	13.1	232	4 US-10-038-854-96	Sequence 66, Appli
14	198	13.1	232	4 US-10-193-452-36	Sequence 36, Appli
15	198	13.1	232	4 US-10-193-452-87	Sequence 87, Appli
16	197	13.1	217	4 US-10-051-874-95	Sequence 95, Appli
17	193	12.8	224	4 US-10-044-564-303	Sequence 30, Appli
18	193	12.8	224	5 US-10-044-564-303	Sequence 303, Appli
19	191.5	12.7	272	5 US-10-211-028-8	Sequence 8, Appli
20	189	12.6	251	4 US-10-068-134-4	Sequence 4, Appli
21	185.5	12.3	233	4 US-10-056-744B-4	Sequence 4, Appli
22	183.5	12.2	251	3 US-09-099-322-03	Sequence 6126, Appli
23	183.5	12.2	251	5 US-10-494-675-50	Sequence 50, Appli
24	183	12.1	289	5 US-10-732-859-6	Sequence 6, Appli
25	181.5	12.0	264	4 US-10-724-972A-7349	Sequence 7349, Appli
26	180.5	12.0	258	4 US-10-282-122A-70509	Sequence 70509, Appli
27	180.5	12.0	310	4 US-10-425-115-292028	Sequence 292028,

RESULT 2
US-10-033-078-10

; Sequence 10, Application US/100333078
; Publication No. US2002012310941
; GENERAL INFORMATION:

i APPLICANT: Furuchi, Yashiro
 i APPLICANT: Hoshino, Tatsuo
 i APPLICANT: Kimura, Hitoshi
 i APPLICANT: Kiyasu, Tatsuya
 i APPLICANT: Nagahashi, Yoshie
 i TITLE OF INVENTION: BIOTIN BIO-SYNTHETIC GENES
 i FILE REFERENCE: Biotin Genes
 i CURRENT FILING DATE: 2001-12-27
 i PRIOR APPLICATION NUMBER: 09/584,185
 i PRIOR FILING DATE: 2000-06-14
 i NUMBER OF SEQ ID NOS: 23
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO: 10
 i LENGTH: 267
 i ORGANISM: Kurthia sp.
 i US-10-033-078-10

Query Match 20.8%; Score 314.5; DB 4; Length 267;
 Best Local Similarity 33.1%; Pred. No. 2.9e-23;
 Matches 92; Conservative 43; Mismatches 104; Indels 39; Gaps 9;

Qy 1 MAQVKANGITLLEYEBCGHRHPSMILIMGGQLIDWPEEFTRGLAERGRFVICFDNDBA 60
 Db 1 MPFVNHDNESLYEV-HGQGDPLIIMGGYNSLSW-HRTVPTLKR-FKVTFDNRGV 56
 Qy 61 GLSTKLEGVKPNIARVFLASMGKXPRVPYTLDDMALDTVGMLDAGIESTHVGYSMG 120
 Db 57 GKSS--KPEQYSIEMMAEDARAVILDAVSDAHYGISING 95
 Qy 121 GMIAOILGAKHGERVYSLTMITSSGNPMPAPRPOV--LQKEMRVPKSMDREW--- 173
 Db 96 GMIAQRLLATYPVRSVLVGCCTAGGTHIQPSPISTLMVRASLTGSQRTSNE-LDKINI 208
 Qy 174 IKNUELLTTIGSPGLDREKLALDVRKSITERCLCDEGTORQLAATLQSRSRVKLLRIAV 233
 Db 156 IVYQSAPIEK-HPELQS---DIQRKELEITPPSAYLSQLQACLTHTSNE-LDKINI 208
 Qy 234 PTLVSGAEDPLPYOCBDRDADHHPGARFELIEGMGH 271
 Db 209 PTLVHGDAEMLVPGMHLAERIQGSQHTVSCAGH 246

RESULT 4
 US-10-211-028-165
 ; Sequence 165; Application US/10211028
 ; Publication No. US20050027113A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CUBIST PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAFTOMYCIN
 ; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER
 ; FILE REFERENCE: CUB-12 PCT CIP
 ; CURRENT APPLICATION NUMBER: US/10/211,028
 ; CURRENT FILING DATE: 2004-07-31
 ; PRIOR APPLICATION NUMBER: PCT/US02/24310
 ; PRIOR FILING DATE: 2002-10-25
 ; PRIOR APPLICATION NUMBER: PCT/US01/32354
 ; PRIOR FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 60/310,385
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: 60/379,866
 ; PRIOR FILING DATE: 2002-05-10
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 165
 ; LENGTH: 273
 ; TYPE: PRT
 ; ORGANISM: Streptomyces coelicolor
 US-10-211-028-165

Query Match 17.8%; Score 268.5; DB 5; Length 273;
 Best Local Similarity 26.8%; Pred. No. 1.5e-18;
 Matches 85; Conservative 44; Mismatches 109; Indels 79; Gaps 10;

Qy 1 MAQVKANGITLLEYEBCGHRHPSMILIMGGQLIDWPEEFTRGLAERGRFVICFD 56
 Db 1 MPVLTNGRINYDDAPPAGAQAPAVLVMGSSGSRGAWHLHQPAVLAAGFRVTSDF 60
 Qy 57 NRDAGLSTKLEGVKPKNIARVFLASMGKXPRVPYTLDDMALDTVGMLDAGIESTHVG 116
 Db 61 NRGIAPSEEPG---GFGIDLVDVADTAALVEERLGPGRVAG 99
 Qy 117 VSMGMAQILGAKHGERVYSLTIMITSSGNP-----RMPAPRPOV 157
 Db 100 ISMGSAHIAELALSRPDLVDRLVMTA-RPDALREALGRAEMBLQGDRSKLADWKS1ERCLCBEQTQ 212
 Qy 158 LQKPMVR-PKSMDKE---EWIKNLLELTIGSPGLDRSKLADWKS1ERCLCBEQTQ 212
 Db 159 VQAMQNLSPRTLNDVQADWLDV-LETTRSSGA-----G-YR 194

RESULT 3
 US-10-763-933-10
 i Sequence 10, Application US/10/63933
 i Publication No. US20040137584A1
 i GENERAL INFORMATION:
 i APPLICANT: Furuchi, Yashiro
 i APPLICANT: Hoshino, Tatsuo
 i APPLICANT: Kiyasu, Tatsuya
 i APPLICANT: Nagahashi, Yoshie
 i TITLE OF INVENTION: BIOTIN BIO-SYNTHETIC GENES
 i FILE REFERENCE: Biotin Genes
 i CURRENT APPLICATION NUMBER: US/10/763,933
 i CURRENT FILING DATE: 2004-01-23
 i PRIOR APPLICATION NUMBER: US/10/033,078
 i PRIOR FILING DATE: 2001-12-27
 i PRIOR APPLICATION NUMBER: 09/594,185
 i PRIOR FILING DATE: 2000-06-14
 i PRIOR APPLICATION NUMBER: EP 96115540.5
 i PRIOR FILING DATE: 1996-09-27
 i NUMBER OF SEQ ID NOS: 23
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO: 10
 i LENGTH: 267
 i TYPE: PRT
 i ORGANISM: Kurthia sp.
 i US-10-763-933-10

SOFTWARE: PatentIn version 3.0
 SEQ ID NO 18
 LENGTH: 264
 TYPE: PRT
 ORGANISM: Streptomyces fradiae
 US-10-329-079-18

Query Match 14.3%; Score 216.5; DB 4; Length 264;
 Best Local Similarity 25.8%; Pred. No. 2.9e-13; Mismatches 44; Indels 10;
 Matches 79; Conservative 44;

Qy 5 KANGITLLEYEEQGRHRHPSMMLIMGLGGQLIDWPEFIRGLAERGFRVVICFDNRDAGLST 64
 Db 4 RINGIDDLHERRG--SGSPVILLMSGAATGFWHLHQVPAVALVAAGFEAVTFTRN---- 55

Qy 65 KLEGVKKPNIARVFLASMGKPR--VPTFLDMALDTVGLMDALGISTHVVGVSMCG 121
 Db 56 -----GTPSSGGGPGLQDMAADTGLIHLGHGCAVVGTSLG 96

Qy 122 MIAQILGAKHGGERVKSLSLTMITSSGNPRMPA-----PRPOVLOKEMR- 163
 Db 97 RVACEYARTRPDVLVRCVLMAPRADRTRAATEAIALADSGTVPRYAVRRAVN 156

Qy 164 -VPKSMDEKEENIKYNNEL-LTTTSPGLDREKLAIDVRKSIERCLCPESTQRQLAIIQ 220
 Db 157 LSPRTLADDERIADWDLDFELAAAGPG-----ARTQLBISAYH 196

Qy 221 SGSRVKLLRRIAVPLVIVSGADEPLLPYQGRDIADHPIGARFELIEGNIGH---DIPR 276
 Db 197 --REBEDLARTAPCRVIAFADDIVAPAHAKETADALPSEADYHVVPDQCHYGEQPPR 253

Qy 277 HIPRLI 282
 Db 254 -VNRLII 258

RESULT 8
 US-09-976-059-10
 Sequence 10. Application US/09976059
 Patent No. US2002016447AI
 GENERAL INFORMATION:
 APPLICANT: Farmer, Chris
 APPLICANT: Zazopoulos, Emmanuel
 APPLICANT: Staffa, Alfredo
 TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
 FILE REFERENCE: 3019.PCT
 CURRENT APPLICATION NUMBER: US/09/976,059
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 10
 LENGTH: 271

OTHER INFORMATION: V represents a non-standard initiator codon. It is expected that
 OTHER INFORMATION: the biosynthesized protein will have a formylmethionine residue
 OTHER INFORMATION: at this position
 US-09-976-059-10

Query Match 13.5%; Score 204; DB 3; Length 271;
 Best Local Similarity 25.0%; Pred. No. 5.6e-12; Mismatches 38; Indels 76; Gaps 9;
 Matches 78; Conservative 38;

Qy 4 VKANGITLLEYEEQGRHRHPSMMLIMGLGGQLIDWPEFIRGLAERGFRVICEDNRDAGL 63
 Db 9 VRTNSVYLAIRRSAGE--PYLMIGMSGAGOTVYHOTPALHEAGYSTVNPDSR---- 61

Qy 64 TKLEGVKKPNIARVFLASMGKPRVPTFLDMALDTVGLMDALGISTHVVGVSMCGI 123
 Db 62 ---GIPPSDV-----PAGKYSILADMTPADTRGLIEALDIAPIRIVGTSLGMI 105

Qy 124 AQILGAKHGGERVKSLSLTMITSSGNPRMPA PRPO---YLQKFMRVPKSMDK----- 170
 Db 106 AQELAVDHPFLVRAVLIATLARPDAARAQNQADIDLESVTPLAAVBAATAVPKMFS 165

Qy 171 -----EENIKYNNELTTTIGSPGLDREKLAIDVRKSIERCLCPESTQRQLAIIQ 220
 Db 166 PATINDDYAVREWLDI -PELSGTCVSAG-----GOAWAEI- 199

Qy 221 SGSRVKLLRRIAVPLVIVSGADEPLLPYQGRDIADHPIGARFELIEGNIGH---DIPR 276
 Db 200 TGDRRAALRSVTAPCRVIFADDLITPHLAEEVAAPDCDLYVEISRCGHLGYLERPDA 259

Qy 277 HIPRLIELJAGH 288
 Db 260 VNAAILEFLDSH 271

RESULT 9
 US-10-156-761-8055
 Sequence 8055; Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIOUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-1262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIORITY APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIORITY APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 8055
 LENGTH: 303
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-8055

Query Match 13.5%; Score 204; DB 4; Length 303;
 Best Local Similarity 27.1%; Pred. No. 6.6e-12;
 Matches 76; Conservative 46; Mismatches 102; Indels 56; Gaps 10;

Qy 22 PSMILIMLGQLIDWPBEPFIRGLAERGFRVICEDNRDAGLSTKLEGVKKPNIARVFLA 81
 Db 65 PALIFLHYWGGSRTTWIPLVQLRDQGQF--VAYDQRSWGGSGTSPVPG----- 109

Qy 82 SMGLKPRVPTFLDMALDTVGLMDALGIBSTHVVGSNGGMIAQILGAKHGERVSKSLTM 141
 Db 110 -----PYDLEQLADDAQRVTDALGYSRYLVGHSMGGKVAQILAAARKPAGIRGVVL 161

Qy 142 ITSGSNPMPNMPAPRQVQKEMRVPKSMDEKEENIKYNNELTTG-SPLDREKLAIDVR 199
 Db 162 A---PAPPAPGTVGTVQETVSHADNEAVLQSIDMLPRLRQVEDSLR 216

Qy 200 KSIERCLCPESTQRQLAIIQSGSRVKKLRRIAVPTVYISGARDPLPYQGRDIADH-- 257
 Db 217 GGDBEARL-EWPRLVYDVSAG---VSATEVPVLTAGSHDKVDPPTV--LADHDL 266

Qy 258 --IPGARFELIEGNIGH---DIPR-----HPLRQVTEVPLGHTLPELRRQVEDSLR 291
 Db 267 PLIPTATLVDKTGHLSPLEVDPQ-----VAHIGA 298

RESULT 10
 US-09-96-578-4
 Sequence 4, Application US/09896578
 ; Sequence 4,

Query	Match	13.1%; Score 198; DB 3; Length 232;
Best Local Similarity	31.5%; Pred. No. 1.9e-11;	
Matches	36; Mismatches 90; Indels 52; Gaps 12;	
Qy	50 FRRVICFDNRDGLSTKLEGVKPKPNIAKRVFLASMGKJPRVPTYTLDMALDTVGLMRALGI 109	
Db	1 FRRVILLDRGFGESSSSD-----LAE-----YRFDLDAEDLEALLDGL 40	
Qy	110 ESTHVV-YGVSMCGMIAQILGAKHGE-RVKSLTLMITSSGNPRMPA-----PRPVQLQK 160	
Db	41 EKPVILVGSHSGAIAYAKYPERKRVKLV-----SPPLPAGLSSDLPQRQNLLEG 95	
Qy	161 FM-----RVPKSMDKEWIKYNLELLTTIGSPGL-DREKLALDVRSKSIERCLCPGTQR 213	
Db	96 LLANFRNRLSRV-EALLGRALKQFELLGRPLRYSDFLKQAEDEWSSLTRQGEDDGDG 153	
Qy	214 QLAALILOSSRVK---LLRRIAVPVLVISSAEDPPLPYQCGRDIAHDHPARFEJEGM 269	
Db	154 LIGAAVALGKQWDISALDKIVPFLVINGTDDPLVPLDASEKLSALIPNAEVVVIDDA 213	
Qy	270 GH---DIPERHIPRILELI 285	
Db	214 GHIALLEKPE-EVAEIKFL 232	
RESULT 12		
US-10-289-148-4		
Sequence 4, Application US/10289148		
Publication No. US2010010001A1		
GENERAL INFORMATION:		
APPLICANT: Millennium Pharmaceuticals, Inc.		
APPLICANT: Kapeller-Libermann, Rosana		
APPLICANT: Spurling, Heidi L.		
TITLE OF INVENTION: 46694, A HUMAN ALPHA/BETA HYDROLASE		
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREFOR		
FILE REFERENCE: NPI01-295PR.RNM		
CURRENT APPLICATION NUMBER: US/10/289,148		
CURRENT FILING DATE: 2002-11-06		
PRIOR APPLICATION NUMBER: US 60/334,725		
PRIOR FILING DATE: 2001-11-29		
NUMBER OF SEQ ID NOS: 6		
SOFTWARE: FastSEQ for Windows Version 4.0		
SEQ ID NO 4		
LENGTH: 232		
TYPE: PRT		
ORGANISM: Artificial Sequence		
FEATURE:		
OTHER INFORMATION: Alpha/Beta Hydrolase Fold Consensus Domain		
US-10-289-148-4		
Query Match 13.1%; Score 198; DB 4; Length 232;		
Best Local Similarity	31.5%; Pred. No. 1.9e-11;	
Matches	36; Mismatches 90; Indels 52; Gaps 12;	
Qy	50 FRRVICFDNRDGLSTKLEGVKPKPNIAKRVFLASMGKJPRVPTYTLDMALDTVGLMRALGI 109	
Db	1 FRRVILLDRGFGESSSSD-----LAE-----YRFDLDAEDLEALLDGL 40	
Qy	110 ESTHVV-YGVSMCGMIAQILGAKHGE-RVKSLTLMITSSGNPRMPA-----PRPVQLQK 160	
Db	41 EKPVILVGSHSGAIAYAKYPERKRVKLV-----SPPLPAGLSSDLPQRQNLLEG 95	
Qy	161 FM-----RVPKSMDKEWIKYNLELLTTIGSPGL-DREKLALDVRSKSIERCLCPGTQR 213	
Db	96 LLANFRNRLSRV-EALLGRALKQFELLGRPLRYSDFLKQAEDEWSSLTRQGEDDGDG 153	
Qy	214 QLAALILOSSRVK---LLRRIAVPVLVISSAEDPPLPYQCGRDIAHDHPARFEJEGM 269	
Db	154 LIGAAVALGKQWDISALDKIVPFLVINGTDDPLVPLDASEKLSALIPNAEVVVIDDA 213	
Qy	270 GH---DIPERHIPRILELI 285	
Db	214 GHIALLEKPE-EVAEIKFL 232	

RESULT 13
US-10-038-854-66
; Sequence 66, Application US/10038854
; Publication No. US20040022781A1
GENERAL INFORMATION:
; APPLICANT: Spycer, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Bisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Keruda, Rameah
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangoli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boildog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Ellerman, Shlomit R
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 214012-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,795
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 66
LENGTH: 232
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-854-66

Query Match 13.1% Score 198; DB 4; Length 232;
Best Local Similarity 31.5%; Pred. No. 1,9e-11;
Matches 82; Conservative 36; Mismatches 90; Indels 52; Gaps 12;

RESULT 14
US-10-193-452-36
; Sequence 36, Application US/10193452
; Publication No. US20040214758A1
GENERAL INFORMATION:
; APPLICANT: Meyers, Rachelle E
; APPLICANT: Gluckemann, Maria Alexandra
; APPLICANT: Curtiss, Rory A. J.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN HYDROLASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-194001
; CURRENT APPLICATION NUMBER: US/10/193,452
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US 09/816,664
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,973
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 09/841,880
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,559
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 09/862,556
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: PCT/US01/16424
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/206,036
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/861,165
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/16014
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,442
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/875,353
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18335
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,949
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/896,578
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/20880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/214,948
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/911,150
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/US01/23153
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,008
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/911,317
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/US01/23160

PRIOR FILING DATE: 2001-07-23
 PRIOR APPLICATION NUMBER: US 60/220, 040
 PRIOR FILING DATE: 2000-07-21
 PRIOR APPLICATION NUMBER: US 09/934, 323
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: PCT/US01/26091
 PRIOR FILING DATE: 2001-08-21
 PRIOR APPLICATION NUMBER: US 60/226, 774
 PRIOR FILING DATE: 2000-08-21
 PRIOR APPLICATION NUMBER: US 09/963, 559
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: PCT/US01/29962
 PRIOR FILING DATE: 2001-09-25
 PRIOR APPLICATION NUMBER: US 60/235, 033
 PRIOR FILING DATE: 2000-09-25
 PRIOR APPLICATION NUMBER: US 09/971, 490
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: PCT/US01/31674
 PRIOR FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: US 60/238, 170
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: US 10/071, 275
 PRIOR FILING DATE: 2002-02-07
 PRIOR APPLICATION NUMBER: PCT/US02/03793
 PRIOR FILING DATE: 2002-02-07
 PRIOR APPLICATION NUMBER: US 60/267, 054
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: US 09/888, 911
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: PCT/US01/19967
 PRIOR FILING DATE: 2001-06-25
 PRIOR APPLICATION NUMBER: US 60/213, 688
 PRIOR FILING DATE: 2000-06-23
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 36
 LENGTH: 232
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: consensus sequence
 US-10-193-452-36

FEATURE:
 Query Match 13.1%; Score 198; DB 4; Length 232;
 Best Local Similarity 31.5%; Pred. No. 1.9e-11; Indels 52; Gaps 12;
 Matches 82; Conservative 36; Mismatches 90;

Qy	50	F R V I C F D N R D A G L S T K L E G Y K K P N I A R V F L I A S M G L K P R V P Y T D M A L D T V G I M D A L G I	109
Db	1	F R V I I D L R G F G E S S P D -----LAE-----Y R F D D A E L A I D A L G I	40
Qy	110	E S T H Y - V G V N G G M A Q I L G A X H G E - R V K S I L M T I S S N P R M P A -----P R P Q V D Q R 160	
Db	41	E K P V I L V G H S M G G A T A L A Y A K Y P E R V Q R V L V L V -----S P P L D A G L S S D L P F R Q G N L E G	95
Qy	161	F M -----R V P K S M D K E E W I K Y N U L L T T G S P G L - D R E K L A D O V R K S T E R C L P E G T O R	213
Db	96	L L A N F R N R L S R S V - E A L I G R A L Q F O F I G R P L Y S D F K R Q A E D M L S S I T R Q G D D G G G	153
Qy	214	Q L A T L Q S G R V K -----L L E R I A V P T L V S G A E D P L P V Q C G R D I A D H P G A R P E L I E C M	269
Db	154	L L G R A V A G L Q L Q W D L S A L D K I V P T L V W G T D D L V P D A S E K U S A L I P N A E V V I D D A	213
Qy	270	G H -----D I P E R H I P P I L E I	285
Db	214	G H L A L J E K P E - E V A E L I K F L	232

RESULT 15
 US-10-193-452-87
 ; Sequence 87, Application US/10193452
 ; Publication No. US20040214758A1
 ; GENERAL INFORMATION: PCT/US02/03793

```

; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/267,054
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: US 09/888,911
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/US01/19967
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,688
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 87
LENGTH: 232
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus sequence
US-10-193-452-87

Query Match          13.1% ; Score 198; DB 4; Length 232;
Best Local Similarity      31.5% ; Pred. No. 1,9e-11;
Matches 82;  Conservative 36;  Mismatches 90;  Indels 52;  Gaps 12;

Qy  50 FRVICIDNRDAGLSTKLEGVKKPNIAVFLASMGKLPFRVPYTLDDMDALTYGLMDALGI 109
Db   1 FRVILDLRGRGESSSD-----LAE-----YRFDDIAEDLEAII DALG L 40
Qy  110 ESTHV VGVSNSGGMIOILGAKHGB-RVKSLTLMUTISGGNPMPA-----PRPVQLQK 160
Db   41 EKPVIIVGHSGGAIALAYAKYPERKVALV-----SPPLPGLOSSDLPRQGNLQE 95
Qy  161 FM-----RVPKSMDKEWIKYLNELLTIGSPL-DREKLAIDLVRKSIERCLCPEGTOR 213
Db   96 LLANFNRNLSRSV-EALLGPALKQFFLGRLPVLSSDEFLQKAEDWLSSLIROQEDGDG 153
Qy  214 QLAAALIQSGBVK----LIRRRIAVPTVVISGEDPLPYQCCBDIAHPIGARFELIEGM 269
Db  154 LLGAVALGKGQLQWDISALKDIKVPTLVIGTDDPLVLDASEKSLALIPNAEVVVDDA 213
Qy  270 GH---DIPERHIPRIJELI 285
Db  214 GHATLAKPKP-FVAFITKPF 232

```

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: April 13, 2006, 13:11:49 ; Search time 27 Seconds
(without alignments)

Title: US-10-686-490D-2

Perfect score: 1509

Sequence: MAQVRKANGITLLEYEQGHRH.....ERHPLIELJAGHAAAAEA 294

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:
1: /SDDSS/ptodata/1/pubpa/us08 NEW PUB .pep: *
2: /SDDSS/ptodata/1/pubpa/us06 NEW PUB .pep: *
3: /SDDSS/ptodata/1/pubpa/us07 NEW PUB .pep: *
4: /SDDSS/ptodata/1/pubpa/pct NEW PUB .pep: *
5: /SDDSS/ptodata/1/pubpa/us03 NEW PUB .pep: *
6: /SDDSS/ptodata/1/pubpa/us10 NEW PUB .pep: *
7: /SDDSS/ptodata/1/pubpa/us11 NEW PUB .pep: *
8: /SDDSS/ptodata/1/pubpa/us60 NEW PUB .pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	209.5	13.9	260	7	US-11-087-099-1714		Sequence 1714, Application US-11-087-099-1714
2	204	13.5	271	7	US-11-205-109-10		Sequence 10, AppI
3	201.5	13.4	312	7	US-11-087-099-5676		Sequence 5676, AppI
4	193	12.8	224	7	US-11-054-281-103		Sequence 303, AppI
5	187	12.4	265	7	US-11-087-099-4437		Sequence 4437, AppI
6	183.5	12.2	251	7	US-11-155-822-470		Sequence 470, AppI
7	183	12.1	265	7	US-11-087-099-3057		Sequence 9057, AppI
8	176.5	11.7	266	7	US-11-087-099-367		Sequence 967, AppI
9	176.5	11.7	266	7	US-11-087-099-8501		Sequence 8501, AppI
10	168.5	11.2	293	6	US-10-467-657-6664		Sequence 6664, AppI
11	160	10.6	2197	7	US-11-075-185-8		Sequence 8, AppI
12	155.5	10.3	286	7	US-11-179-977-9		Sequence 9, AppI
13	147	9.7	308	7	US-11-096-568A-256010		Sequence 25601, A
14	147	9.4	330	7	US-11-096-568A-256010		Sequence 25600, A
15	145.5	9.6	264	7	US-11-096-568A-29097		Sequence 29097, A
16	145.5	9.6	307	7	US-11-096-568A-29096		Sequence 29096, A
17	145.5	9.6	311	7	US-11-096-568A-29096		Sequence 29095, A
18	141.5	9.4	256	7	US-11-096-568A-29096		Sequence 29096, A
19	141.5	9.4	267	7	US-11-087-099-11146		Sequence 11146, A
20	141.5	9.4	299	7	US-11-096-568A-29095		Sequence 29085, A
21	141.5	9.4	303	7	US-11-096-568A-29094		Sequence 29084, A
22	136.5	9.0	269	7	US-11-179-977-11		Sequence 11, AppI
23	136.5	9.0	269	7	US-11-087-099-8151		Sequence 8151, AppI
24	135	8.9	311	7	US-11-096-568A-4794		Sequence 4794, AppI
25	130.5	8.6	256	7	US-11-179-977-15		Sequence 15, AppI

RESULT 2

US-11-205-109-10
; Sequence 10, Application US-11-205-109-10
; Publication No. US0050287641A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris

ALIGNMENTS

RESULT 1
US-11-087-099-1714
; Sequence 1714, Application US-11-087-099-1714
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abid, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21 (53450)B EP
; CURRENT APPLICATION NUMBER: US-11-087-099-1714
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1714
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Bradyrhizobium japonicum USDA 110
US-11-087-099-1714

Query Match 13.9%; Score 209.5; DB 7; Length 260;
Best Local Similarity 26.1%; Pred. No. 4,1e-12; Matches 105; Indels 63; Gaps 8;

Matches 74; Conservative 37; Mismatches 105; Indels 63; Gaps 8;

Qy 1 MAQVKANGTILEYEQGHRHHPSMSLIMGLGCCOLIDWPBEFTIRGLAERGFRCIFDNRDA 60
Db 1 MPMDADGCLINVSVEGRDGPTMLNSLGTQLQMN-EPNQNKALTQ-VFVRYDRRGH 58
Qy 61 GLSTKLEGVKRKENIARYPVLASMGMLKBRVPYTLDMALDHALGIESTHVGSMG 120
Db 59 G-----KSNV-----PGPYTMERFGRDVLAINDNIEKVHWGCLSMG 97
Qy 121 GMIAQILGAKHGERVKSLLTLMITSSGNPRMFKNPVRPKVQLQKPMAPRPQVLPKQPMRDKFNRVPSMDKEEMIYNLEL 180
Db 98 GMWQWLGANAEPERFGKLANTSC-----YYAEPTKWW-----LER 133
Qy 181 LTTIGSPGL-----DREKLALDVKRS1ERCLCPEGTORQLA--ILQSGR 224
Db 134 IDAVKRGSIAYAADATAGWLTQDFERREPDTARMKAMLLASPVEGYLACCEBALSTDQ 193
Qy 225 VKLLRRIAVPTLVISGAEDPLLPYQQCGRDIADHPIGARFELIE 267
Db 194 REPLLKIKSPTLVIAGRHDATMPISAGELIRSKIPGANMTID 236

APPLICANT: Zazopoulos, Emmanuel
 APPLICANT: Staffa, Alfredo
 TITLE OF INVENTION: CBNA CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
 FILE REFERENCE: 3002-B-US
 CURRENT APPLICATION NUMBER: US/11/205,109
 PRIOR APPLICATION NUMBER: US/09/976,059
 PRIOR FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: US 60/239,924
 PRIOR FILING DATE: 2000-10-13
 NUMBER OF SEQ ID NOS: 46
 SEQ ID NO: 10
 LENGTH: 271
 TYPE: PRT
 ORGANISM: Actinoplanes sp.
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(1)
 OTHER INFORMATION: V represents a non-standard initiator codon. It is expected that the biosynthesized protein will have a formylmethionine residue at this position
 US-11-205-109-10

Query Match Score 204; DB 7; Length 271;
 Best Local Similarity 25.0%; Pred. No. 1.4e-11;
 Matches 78; Conservative 38; Mismatches 120; Indels 76; Gaps 9;

Qy 1 MAQVANGITLVEEQHRRHPSMLLIMGLGGOLIDWPEEFIRGLAERGFRVICFDNRDA 60
 Db 51 MPHAEIGDRNLNLDDEGATGAPVFAHALGSDRHW -DNLPLPQDLRVRDYLGRH 108
 Qy 61 GLSTKLEGVKKPNIARVFLASNGLKPVRPYTLDMDALDTVGIMDALGIESTHVGVNSG 120
 Db 109 GRST------TPEPPYANGALIINDAERMEALSIREAVFGCSIG 147
 Qy 121 GMIAQILGAKHGERVKSLTLMITSSGNPRMAPPQVQKFMRVPKSMDKBENIK-YNLE 179
 Db 148 GMIAQGLAVKLRLDVLVGLCDTA -----KIGTPETWQ-----DRIDQVRSYGE 193
 Qy 180 LUTTIGSPGLDREKLADPVKSTERCLCP---EGTQRQL-----AAIQ 220
 Db 194 SLAD-----PTMKRWFAFAPAFQGPPEGQWREFBPGDPGYAGGAIA 237
 Qy 221 SGSRVKLIRRIAVPTLVISGAEDPLLPYOCGRDIADHHPGARFELIGMGH 271
 Db 238 GTDFYTTRTARLTLPALVGSEDGSTPDLYRETALIERSREIVRGAGH 288

RESULT 4
 US-11-054-281-303
 Sequence 303, Application US/11054281
 Publication No. US2006001381341
 GENERAL INFORMATION:
 APPLICANT: Mezes et al.
 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 FILE REFERENCE: 21402-240CIP
 CURRENT APPLICATION NUMBER: US/11/054,281
 PRIOR APPLICATION NUMBER: 60/261,014
 PRIOR FILING DATE: 2005-02-08
 PRIOR APPLICATION NUMBER: 60/261,014
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: 60/261,018
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: 60/318,410
 PRIOR FILING DATE: 2001-09-10
 PRIOR APPLICATION NUMBER: 60/261,013
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: 60/261,026
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: 60/261,029
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: 60/313,170
 PRIOR FILING DATE: 2001-08-17
 PRIOR APPLICATION NUMBER: 10,044,564
 PRIOR FILING DATE: 2002-01-11
 NUMBER OF SEQ ID NOS: 324
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO: 303
 LENGTH: 224
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:consensus
 OTHER INFORMATION: sequence
 US-11-054-281-303

Query Match Score 193; DB 7; Length 224;
 Best Local Similarity 28.1%; Pred. No. 1.2e-10;
 Matches 71; Mismatches 31; Indels 80; Gaps 9;

Qy 52 VICFDNDAGLSTKLEGVKKPNIARVFLASNGLKPVRPYTLDMDALDTVGIMDALGIES 111
 Db 1 VILFDLRLFGQSPSPD-----LAB-----YRPDLABEALIDALGLDK 40
 Qy 112 THVGVSMGMAQILGAKHGERVKSLTLMITSSGNPRMAPPQVQKFMRVPKSMD-----168
 Db 41 VILVGHSMGGAATAAAAKYPERVKLV-----VSAPHPALLSSRL-FPRNLFGI 90
 Qy 169 -----DKEEWKYNLELLTIGSPGLDREKLADPVKSTERCLCPBGTQRQLA 217

RESULT 3
 US-11-087-099-5676
 Sequence 5676, Application US/11087099
 Publication No. US20060041361A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO: 5676
 LENGTH: 312
 TYPE: PRT
 ORGANISM: Rhodobacter sphaeroides
 US-11-087-099-5676

Query Match Score 201.5; DB 7; Length 312;
 Best Local Similarity 24.4%; Pred. No. 3e-11;
 Matches 71; Conservative 42; Mismatches 105; Indels 73; Gaps 8;

Db	91	LILANPRNRLRSVEALLBALKQFFLIGRP-----IVSDFLKQE	--LSS 133
Qr	218	IILQSG-----SRVYL-----LRRIAVPTLYTISGARDPLLPYQCGRDIADHI 258	
Qr	134	LIRFGEDDDGGDGILLWALQKLQWDSADLRKRVPTLVGGDDPLVPPDAEKSLSALP 193	
Qy	259	PGEARFELTEGMGH 271	
Db	194	PNAEVVVIDDAGH 206	
RESULT 5			
	US-11-087-099-4437		
	Sequence 4437, Application US/11087099		
	Publication No. US20060041961A1		
	GENERAL INFORMATION:		
	APPLICANT: Abad, Mark S. et al.		
	TITLE OF INVENTION: Genes and Uses for Plant Improvement		
	FILE REFERENCE: 38-21(5345)0 B EP		
	CURRENT APPLICATION NUMBER: US/11/087, 099		
	CURRENT FILING DATE: 2005-03-22		
	NUMBER OF SEQ ID NOS: 12464		
	SEQ ID NO: 4437		
	LENGTH: 265		
	TYPE: PRT		
	ORGANISM: Agrobacterium tumefaciens		
	STR. C58 (Cereon)		
	US-11-087-099-4437		
Qy	Query Match 12.4%; Score 187; DB 7; Length 265;		
	Best Local Similarity 28.0%; Pred. No. 5,66-10;		
	Matches 83; Conservative 36; Mismatches 89; Indels 88; Gaps 12;		
Db	22 PSMLILNGGOLIDWPBEFIRGLAERGLDAGLIEESTHVGGSNCMIAQLGAGCHGERVSKSLTM 141		
Qy	23 PVIAFINSLGTDPRI-DAVIAEGD-DIAYVLLDKDRGHGLS----- 62		
Db	82 SMSGKLKPVRYPYTLDDMALDTVGLMDALGIEESTHVGGSNCMIAQLGAGCHGERVSKSLTM 141		
Qy	63 DVG--RAPSIDDHAGDLIADLHDLEIKSAVIGLWSVCGLIAGQYARRPDLYVALRLLS 119		
Db	142 ITSS--GNPRMPAPRQVQLQKFMRVPKSNDKEEMIKYNLELLITGSPGLDREKLALDVR 199		
Qy	120 NTAAHRIGTEMNAR-----IDK-----IAADG-----IASLYVD 148		
Db	200 KSIERCLCPGTORQLAATLQSGSRVKLLR-----RIAVPTL 236		
Qy	149 PWMBRWTTPAFROREAA-YAGRNMLSQPEAGYSGTCAIRDADFTEQAGRIAVPAL 206		
Db	237 VISGAEDPLPYCQGRDIAHDIFGARFELIEJEGMHDPERHPIRLIE-LIAGHAA 291		
Qy	207 C1AGQDQGSTPPSLVQSLAGLIPKSRFTVIAGG-----HIPCIEQPLVYQAQS 256		
RESULT 6			
	US-11-055-822-470		
	Sequence 470, Application US/11055822		
	Publication No. US20050260707A1		
	GENERAL INFORMATION:		
	APPLICANT: Pondejus, Markus		
	APPLICANT: Kroger, Burkhard		
	APPLICANT: Schroder, Hartwig		
	APPLICANT: Zelzer, Oskar		
	APPLICANT: Haberhauer, Gregor		
	TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING		
	TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS		
	FILE REFERENCE: BG1-12LCPCN		
	CURRENT APPLICATION NUMBER: US/11/055, 822		
	CURRENT FILING DATE: 2005-02-11		
	PRIOR APPLICATION NUMBER: 09/606, 740		
	PRIOR FILING DATE: 2000-06-23		
	PRIOR APPLICATION NUMBER: 60/141, 031		
	PRIOR FILING DATE: 1999-06-25		
	PRIOR APPLICATION NUMBER: 60/142, 101		

Qy 82 SMGLKPRVPYTLDDMALLDVTGMLMDALIGESTHVGSMGMAQILGAKHGERVKSLLTM 141
 Db 63 DVG---RAPYSPIDDDHGDLLAILEDLBEIKRAVIWLSPGULLAQYLARPPDVALLIS 119
 · Qy 142 ITSS--GNPRAPIAPRQVLQKFMRVPSKMDKEWIKNLLTITGSPGLDREKLALDVR 199
 Db 120 NTAAHRLGTTENWNR----IDK-----IAADG----LASLV 148
 Qy 200 KSIERCLCPGTORQOLAALOSSRSRVKLRL-----RIAVPTL 236
 Db 149 PVMERKFTPAFQRENTA--YAGARNMLSOOPEAGYSGTCAIRDAFFEQAGRIAVPL 206
 Qy 237 VLSGAEDPLPYOCGRDIAHDHPGARFELLEGMDHDIPIERHPIPLIE-LJAGHAA 291
 Db 207 CIAGDQDGPPEPLVOSLAGUPIPKSRFUTAGCG----HIPCLEQPVYYAGRAS 256

RESULT 8
 US-11-087-099-967
 ; Sequence 967, Application US/11087099
 ; Publication No. US20060041961A1
 ; GENERAL INFORMATION
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(53450)B EP
 ; CURRENT APPLICATION NUMBER: US-11/087,099
 ; CURRENT FILING DATE: 2005-03-22
 ; NUMBER OF SEQ ID NOS: 12464
 ; SEQ ID NO: 967
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter calcoaceticus

US-11-087-099-967

Query Match 11.7%; Score 176.5; DB 7; Length 266;
 Best Local Similarity 24.7%; Pred. No. 5.5e-09; Mismatches 45; Indels 61; Gaps 11;
 Matches 71; Conservative 45; Mismatches 110; Indels 61; Gaps 11;

Qy 8 GITLEYEEOGHRHPSMLIMLGQLIDWPPEEFIRGLAERGFVICFDDNDRAGLSTKLE 67
 Db 14 GKTLSVQINGPENAIVPSNSLIGTDHGMWQPO-VAALKSQ-TRVTVTDTRGHGQSDVIE 71
 Qy 68 GVKKPNIAREVFLASMGMLKPRVPYTLDMDALDTVGMLDAGIESTHVGSMGMAQIL 127
 Db 72 NT-----TLDONGEDVDILDLNNTKAHFCCISGGLTALWL 109
 Qy 128 GAKHGERVKSLLT-----MITSSG-NPMPAPRPQVLQKFMRVPKS--MDKBEWIYN 177
 Db 110 GIYQAARPYSITVANSAAKIWEDGWNAABAEVANGLADLVASTHTRWFSDFKDYKNDN 169
 Qy 178 LELTTIGSPGLDREKLALDVRKSIERC--LCPEGTORQOLAALOSSRSRVKLRLRIAVPT 235
 Db 170 L-----AQTIQSLADTPAGYANCRALAKADYREK-LASISIPT 209

RESULT 10
 US-10-467-657-6664
 ; Sequence 6664, Application US/10467657
 ; Publication No. US201005260581A1
 ; GENERAL INFORMATION
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEAR ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIORITY APPLICATION NUMBER: GB-0103424.8
 ; PRIORITY FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO: 6664
 ; LENGTH: 293
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-6664

Query Match 11.2%; Score 168.5; DB 6; Length 293;
 Best Local Similarity 27.5%; Pred. No. 3.6e-08; Mismatches 44; Indels 41; Gaps 11;
 Matches 64; Conservative 44; Mismatches 84; Indels 41; Gaps 11;

Qy 72 PNIA-RVFLASMG-----LKPRPYTLLDDMADJTVGLMDA-----LGIB-----110
 Db 46 PDAAKTYLILHGWNHAFDDLMPLRIPATNPVSADLPGHGDAPFAQPFDEAAADGIA 105

Qy 111 -----STHVVGSMGMAQITGAKHGERVKSLLT-----MITSGGNPR-MPAPRQVL 158
 Db 106 AQDTDSADLGSVLSGGINVALYAARPDVKVRSCLTASFARITAADYDPEGIAAP--AL 162

Qy 159 QKFMRVPKMSDKGEWIKNLLTITGSPGLDREKLALDVRKSIERCPEGTQRQLAII 218
 Db 163 GRMVGAFT-DYAKH1KOFLO-LQHHTP--DAAEITGRILPDLARCTGTPQALQELDAA 218

Qy 219 LOSGSRYKLLRRIAVPTLVISSGAEDPLPYOCGRDIAHDHPGARFELJEGMHS 271
 Db 219 ERADAR-HLLDKIDDPVYLLVFGKGDALTPLRMGEYIHLRHLKSRUYMEKAH 270

RESULT 9
 US-11-087-099-8501
 ; Sequence 8501, Application US/11087099
 ; Publication No. US20060041961A1
 ; GENERAL INFORMATION
 ; APPLICANT: Abad, Mark S. et al.
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement
 ; FILE REFERENCE: 38-21(53450)B EP
 ; CURRENT APPLICATION NUMBER: US-11/087,099
 ; CURRENT FILING DATE: 2005-03-22
 ; NUMBER OF SEQ ID NOS: 12464
 ; LENGTH: 266
 ; TYPE: PRT

RESULT 11
US-11-075-185-B
Sequence 8, Application US/11075185
GENERAL INFORMATION:
APPLICANT: REEVES, CHRISTOPHER D
APPLICANT: REID, RALPH
APPLICANT: JULIEN, BRYAN
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 8
LENGTH: 2197
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-11-075-185-B

Query Match 10.6%; Score 160; DB 7; Length 2197;
Best Local Similarity 26.4%; Pred. No. 3.9e-06;
Matches 53; Conservative 27; Mismatches 87; Indels 34; Gaps 2;

Db 87 PRVPTLDMDALDTVGLMDALGIBESTHVVYGVSMGGMIAQILGAHKGERVSLTLMITSSG 146
Db 1298 PRGEITMDFTVROVEGVRSQSLGSSVVLVGSFGLVAVAYAOPERSKLVLACTISD 1357
Db 147 NPMRPAAPRQVQLQKPMRVPKSMDREWIKNLLELTISPGLDREKLADVRKSIERCL 206
Db 1358 PASVNGMHLVAEEAQRPDGL-----RALQFADVSKF---- 1390

Db 207 CPEGTQRQLAAILOQSRSRQLRRRIAVPVLIVSAGEDPLPYQCGRDIADHIGARFEI 266
Db 1391 -----PLXSQLSTRLPRLPETLAYPAIPLIVAGEDRVYPTIHAERLRAANPATLHV 1443

Db 267 EGMGDHIPERHPIPRLIELAG 287
Db 1444 EGAGHFLGLSHGGVVLHLYNG 1464

RESULT 12
US-11-179-977-9
Sequence 9, Application US/11179977
Publication No. US20050249789A1
GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
FILE REFERENCE: GC511-PCT
CURRENT APPLICATION NUMBER: US/11/179,977
CURRENT FILING DATE: 2005-07-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 9
LENGTH: 286
TYPE: PRT
ORGANISM: Bacillus
US-11-179-977-9

Query Match 10.3%; Score 155.5; DB 7; Length 286;
Best Local Similarity 21.6%; Pred. No. 5.8e-07;
Matches 63; Conservative 44; Mismatches 130; Indels 59; Gaps 8;

Db 4 VKANGITLKEYEBOQGLLPSMLIMGLGGQLIDWPEEFGLAERGFVICFDNRDAGIS 63
Db 9 VNTNGITLHYAAGREDGIPLIVLHGFFPEWYGMKNO-IKPVLDAGYTAPORGNTMS 67
Db 64 TKLEGVYKPNJARVLLASNLKPKRVPYTLDDMAIGESTHVGSMGMI 123

RESULT 13
US-11-096-568A-25601
Sequence 25601, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO: 25601
LENGTH: 308
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Ceres Seq. ID no. 13492535
US-11-096-568A-25601

Query Match 9.7%; Score 147; DB 7; Length 308;
Best Local Similarity 23.1%; Pred. No. 4.1e-06;
Matches 76; Conservative 52; Mismatches 123; Indels 78; Gaps 13;

Db 3 QVKANGITLKEYEBOQ--HRHHPSMLIMGLGGQLIDWPEEFGLAERGFVICFDNRDAG 60
Db 8 QUEANGITMVAEAGPVNANASPAVLFVHGFPELWYSWRHQ-MGYLAAARGYRCVAPDLRQE 66

Db 61 GLSTKLEGVTKENIARVLLASNLKPKPVP--YTLDMDALDTVGLMDALGIBESTHVGYS 118
Db 67 GGTT-----APEPSTSIVHVGDIVALDHALHPQFYVGH 105

Db 119 MGGMIAQIQLGAKHGERVSKLTMITSSGNPRMPAPRQVQKF--MRVPKSM 168

Db 106 WGAIVSMWNLCLRPDRVAL-WNLSVAMPMPREPQVKP--LETPRANIGDEYYTCRQEQC 162

Db 169 DKREWIKYNLELTTI-----GSPGLDREKLADLVRKSIERCLCPESTORQLAAILQS 221
Db 163 LEAEFATEPDLKSPFTLALTTRATGSSAANDLRKQTYSKOMVLPWSLSSBDSVSYASVSK 222

Db 222 ---GSRVKLRL-----RIAVPFLIVSGRADPLPKYCGRDIADHIGARF 263
Db 223 TGFGAGGNYYCRUDLNWELMAPTGAKVQVPKFIVG-----DSDDLAVHPPGVKR 272

Db 264 ELIEGMGHIDPERHPIPLJELIAGHAAA 292
Db 273 YIHKG-GF---KKDVPMLBEVVVIGAGA 297

RESULT 14
US-11-096-568A-25600
Sequence 25600, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide:

TITLE OF INVENTION: Therby
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096, 568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 25600
 LENGTH: 330
 TYPE: PRT
 ORGANISM: Zea mays subsp. maya
 NAME/KEY: misc_feature
 LOCATION: (1) (330)
 OTHER INFORMATION: Ceres Seq. ID no. 13492534
 US-11-096-568A-25600

Query Match Score 9.7%; Score 147; DB 7; Length 330;
 Best Local Similarity 23.1%; Pred. No. 4.5e-06;
 Matches 20; Conservative 52; Mismatches 123; Indels 78; Gaps 13;

Query 3 QVKANGITLLEEQG--HRHPPSMILLIMGGQLIDWPEEFIRGLAERGRFRVICFDNRDA 60
 Db 30 QLBANGITMVAEAGPVNAAPAVLFVHGPELWYIWSRHG-MGYLAARGRCVAPDLRGY 88

Search completed: April 13, 2006, 13:14:56
 Job time : 28 secs

Query 61 GLSPLKLEGVKKPNTARVELLASMGLKPKRP--YLDMDALDTVLMDALIGESTHIVGS 118
 Db 89 GGT-----APPETTSVTFHTVGDIVALLDHALPOVFWVHD 127

Query 119 MGGMIAQILGAHKGERVKSIITLMITSQGNRMPAPRQPVLQKF-----MRVPKSM 168
 Db 128 WGATVSNWNLCLLDRVRAL-VNLSVAFNRRPCKP--LEYFRAAYGBEYYTCRFQDPG 184

Query 169 DKEEWIKYNELLTII-----GSPGLDREKLADLVRSKIERCICPCGTQROLAALQS 221
 Db 185 LEAFPATFDKSFTTLATRGSAMDIRKOMOTYSKOMVLPWLSEEDVSYIASVSK 244

Query 222 --CSRVKLRL-----RINPDTLISGAEDPLLYQCGRDIAHWIGARF 263
 Db 245 TGFAGGVVNTYRCDDLNWELMAPWTGAKVQVPTKFVG-----DGDLATHHPGVKR 294

Query 264 ELIEGMGHDIPERHIFRLIELIAGHAAA 292
 Db 295 YIHKG-GF--KRDVPMLEEVVVIKGAGA 319

RESULT 15
 US-11-096-568A-29097
 Sequence 29097, Application US/11096568A
 Publication No. US20060043240A1
 GENERAL INFORMATION:
 APPLICANT: Alexandrov, Nickolai et al.
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 FILE REFERENCE: 2750-1592PUS2
 CURRENT APPLICATION NUMBER: US/11/096, 568A
 CURRENT FILING DATE: 2005-04-01
 NUMBER OF SEQ ID NOS: 34471
 SEQ ID NO 29097
 LENGTH: 264
 TYPE: PRT
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: (1) (264)
 OTHER INFORMATION: Ceres Seq. ID no. 3659149
 US-11-096-568A-29097

Query Match Score 9.6%; Score 145.5; DB 7; Length 264;
 Best Local Similarity 25.2%; Pred. No. 4.5e-06;
 Matches 69; Conservative 34; Mismatches 11; Indels 57; Gaps 9;

Query 18 HRHPPSMILLIMGGQLIDWPEEFIRGLAERGRFRVICFDNRDGLSTLEGYKKPNTARV 77
 Db 19 NRKEPNLIAAHGFANAMMOYGBHLRAFGTR-ENVYVBDLFFGLSSSTSE----PRNTES 64